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OM protein - protein search, using sw model

Run on: February 25, 2004, 06:36:35 ; Search time 54 Seconds

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : A_Geneseq_29Jan04;*

1: Geneseqp1980s;*
2: Geneseqp1990s;*
3: Geneseqp2000s;*
4: Geneseqp2001s;*
5: Geneseqp2002s;*
6: Geneseqp2003as;*
7: Geneseqp2003bs;*
8: Geneseqp2004s;*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	81	98.8	15	3 AAY49296	Bay49296 19P2 liga
2	77	93.9	15	2 AAW31400	AAw31400 Synthetic
3	77	93.9	15	2 AAW97230	AAw97230 C-terminal
4	72	87.8	15	3 AAY49293	AAy49293 19P2 liga
5	72	87.8	20	2 AAW31394	AAw31394 Human typ
6	72	87.8	20	3 AAY49294	AAy49294 19P2 liga
7	72	87.8	20	3 AAB10365	Aab10365 Human oxy
8	72	87.8	20	3 AAB90998	Aab90998 Prolactin
9	72	87.8	20	4 AAC62534	Aag62534 Human CRH
10	72	87.8	20	4 AAC62534	Aag62534 Human CRH
11	72	87.8	20	5 AAB26404	Aab26404 Human PrR
12	72	87.8	20	6 ABU60846	Abu60846 Peptide P
13	72	87.8	21	2 AAW61395	AAw61395 Human typ
14	72	87.8	21	3 AAB10366	Aab10366 Human oxy
15	72	87.8	21	4 AAC62535	Aag62535 Human CRH
16	72	87.8	21	6 ABU50847	Abu50847 Peptide P
17	72	87.8	22	2 AAW11396	AAw11396 Human typ
18	72	87.8	22	3 AAB10367	Aab10367 Human oxy
19	72	87.8	22	4 AAG2536	Aag2536 Human CRH
20	72	87.8	22	6 ABU60848	Abu60848 Peptide P
21	72	87.8	30	3 AAY49299	AAy49299 19P2 liga
22	72	87.8	31	2 AAW31391	AAw31391 Human typ
23	72	87.8	31	2 AAW72335	AAw72335 Human typ
24	72	87.8	31	3 AAY49291	AAy49291 19P2 liga
25	72	87.8	31	3	

ALIGNMENTS

RESULT 1
ID AAY49296
XX

AAw31393 Human typ
Aab10364 Human oxy
AAG62533 Human CRH
Abu60845 Peptide P
AAw31390 Human typ
Aaw97226 Human typ
Aab10361 Human oxy
AAG62530 Human CRH

AC AAY49296;
DT 22-FEB-2000 (first entry)
XX
DE 19P2 ligand peptide fragment.
XX
KW Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
KW pituitary; regulatory mechanism; central nervous system; pancreatic.
XX
Homo sapiens.
XX
FH Key
FT Modified-site
FT
FT
XX
PN WO960112-A1.
XX
XX
PD 25-NOV-1999.
XX
XX
XX
PR 21-MAY-1998;
XX
PA (TAKA) TAKEDA CHEM IND LTD.
XX
PI Matsumoto H, Kitada C, Hinuma S;
DR WPI; 2000-03381/03.
XX
PT New monoclonal antibodies, useful in diagnosis, as drugs and in studying
diseases related to ligand abnormality.
XX
Disclosure: Page 27; 73pp; Japanese.

The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in classifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand

Qy	1 CAYWASGRGIRPVGR 14	DE	Human type G protein-coupled receptor ligand fragment 4.
Db	1 CAYWASGRGIRPVGR 14	KW	G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.
		KW	
		KW	
		XX	
		OS	Homo sapiens.
		XX	W09724436-A2.
		XX	PN
		XX	10-JUL-1997.
		PD	
		XX	96WO-JP003821.
		PF	
		XX	26-DEC-1996;
		PR	95JP-0034371.
		PR	28-DEC-1995;
		PR	95JP-00059419.
		PR	15-MAR-1996;
		PR	96JP-0021105.
		PR	12-AUG-1996;
		PR	18-SEP-1996;
		XX	96JP-00246573.
		PA	(TAKA) TAKEDA CHEM IND LTD.
		XX	
		PI	Hirunuma S, Habata Y, Kawamata Y, Hosoya M, Fujii R, Fukusumi S;
		PI	Kitada C;
		XX	
		DR	WPI: 1997-363672/33.
		DR	N-PSDB; AAV02431.
		XX	Ligand Peptide for G protein-coupled receptor - acts by modulating PT function in the central nervous system, pancreas and pituitary gland.
		PS	Claim 2; Page 185; 258pp; English.
		XX	This sequence represents a Peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the CC sequence represented in AAV31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a prophylactic CC or therapeutic agent for dementia, depression, hyperkinetic syndrome, CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, CC growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, CC hypercholesterolaemia, hyperglycidaemia, hyperprolactinaemia, diabetes, CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, CC rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, CC amyotrophic lateral sclerosis, acute myocardial infarction, infertility, CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, CC osteoporosis and/or oligogalactia. Assays can also be developed to screen CC compounds which are capable of altering the binding activity of the CC ligand affecting activation of the G protein-coupled receptor protein CC Sequence 20 AA;
		SQ	Query Match 87.8%; Score 72; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 1.5e-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2 AWYASGRGIRPVGR 14	Qy	2 AWYASGRGIRPVGR 14
Db	2 AWYASGRGIRPVGR 14	Db	7 AWYASGRGIRPVGR 19
		RESULT 6	
		ID	AAW97236
		XX	
		AC	AAW97236;
		XX	
		DT	06-MAY-1999 (first entry)
		XX	Human type ligand polypeptide fragment.
		DE	
		XX	
		RW	Rat type ligand; modulation; prolactin secretion;

KW	G protein-coupled receptor; GPCR; hypocoerianism; gonecyst cacogenesis;	XX	OS	Homo sapiens.
KW	menopausal syndrome; euthyroid; hypometabolism; lactation;	XX	AC	
KW	pituitary adenomatoisis; brain tumour; emmeniopathy; autoimmune disease;	AC		
KW	prolactinoma; infertility; impotence; amenorrhea; Galactorrhea;			
KW	acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome;			
KW	Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;			
KW	contraceptive; placental function; choriocarcinoma; hydroid mole;			
KW	irruption mole; abortion; unthrifly fetus; abnormal sacccharometabolism;			
KW	abnormal lipidmetabolism; oxytocia.			
XX				
OS	Homo sapiens.			
PN	WO958962-A1.			
XX				
PD	30-DEC-1998.			
XX				
PF	22-JUN-1998; 98WO-JP002765.			
XX				
PR	23-JUN-1997; 97JP-00165437.			
XX				
PA	(TAKE) TAKEDA CHEM IND LTD.			
XX				
PI	Hinuma S, Kawamata Y, Fujii R, Matsumoto H;			
XX				
DR	WPI; 1999-105614/09.			
XX				
PT	Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy.			
XX				
PS	Claim 3; Page 166: 241pp; English.			
XX				
CC	The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing for hypocoerianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can be used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, Chiari-Frommel syndrome, Argonz-del Castillo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydroid mole, irruption mole, abortion, unthrifly fetus, abnormal sacccharometabolism, abnormal lipidmetabolism or oxytocia			
XX				
SQ	Sequence 20 AA;			
Query Match	87.8%; Score 72; DB 3; Length 20;			
Best Local Similarity	100.0%; Pred. No. 1.5e-05;			
Matches	13; Conservative 0; Mismatches 0;			
Indels	0; Gaps 0;			
DB	2 AWYASRGIRGPVGR 14			
Db	7 AWYASRGIRGPVGR 19			
RESULT 7				
ID	AAV49294 standard; peptide, 20 AA.			
XX				
AC	AAV49294;			
XX				
DT	22-FEB-2000 (first entry)			
XX				
DB	19P2 ligand peptide fragment.			
XX				
KW	Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.			
KW				

XX Matsumoto H, Kitada C, Hinuma S;
 PI WPI: 2000-452288/39.
 DR
 XX Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
 XX Disclosure; Page 63; 72pp; Japanese.
 XX This invention describes novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion promoter.
 XX SQ Sequence 20 AA;
 Query Match 87.8%; Score 72; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; N-matches 0; Indels 0; Gaps 0;
 QY 2 AWYASRGIRPVGR 14
 DB 7 AWYASRGIRPVGR 19

RESULT 9
 AAB9092 ID AAB9092 standard; peptide; 20 AA.
 XX AC AAB9092;
 XX DT 22-JUN-2001 (first entry)
 XX DB Prolactin releasing peptide SEQ ID NO:166.
 XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX OS Homo sapiens.
 XX CS Synthetic.
 XX EN WO200069900-A2.
 XX PD 23-NOV-2000.
 XX PF 17-MAY-2000; 2000WO-US013576.
 XX PR 17-MAY-1999; 99US-0134446P.
 XX PR 10-SEP-1999; 99US-0153446P.
 XX PR 15-OCT-1999; 99US-015973P.
 XX PA (CONJ-) CONJUCHEM INC.
 XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX DR WPI: 2001-11205/12.
 XX Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
 XX Disclosure; Page 244; 733pp; English.
 XX The present invention describes a modified therapeutic peptide (I) and a comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxy/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interfere with physiological processes.
 CC AAB90839 to AAB9441 represent peptides which can be used in the exemplification of the present invention

Sequence 20 AA;
 Query Match 87.8%; Score 72; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; N-matches 0; Indels 0; Gaps 0;

RESULT 10
 ARG62534 ID AAG62534 standard; peptide; 20 AA.
 XX AC AAG62534;
 XX DT 24-AUG-2001 (first entry)
 XX DE Human CRH releasing protein related peptide SEQ ID NO: 35.
 XX ID Human CRH releasing hormone; CRH; G protein receptor ligand;
 KW Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; hypoadrenocorticism; KW analgesic; hyperadrenocorticism; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
 XX OS Homo sapiens.
 XX PN WO200135984-A1.
 XX PD 25-MAY-2001.
 XX PR 17-NOV-2000; 2000WO-JP008119.
 XX PR 18-NOV-1999; 99JP-00327900.
 XX PR 26-SEP-2000; 2000JP-00297073.
 XX PA (TAKA) TAKEDA CHEM IND LTD.
 XX PI Kitada C, Matsumoto H, Hinuma S;
 XX DR WPI; 2001-355552/37.
 XX PT Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion.
 XX PS Claim 4; Page 75; 90pp; Japanese.
 XX CC The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion, such as hyperadrenocorticism, Addison's disease (including bordom, nausea, pigmentation, hypogonadism, hair loss, and hypertension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the invention

therapeutic agent.

XX

Homo sapiens.

OS

WO9724436-A2.

PN

XX

10-JUL-1997.

XX

26-DEC-1996;

XX

96WO-JP003821.

PR

28-DEC-1995;

XX

95JP-00343371.

PR

96JP-00059419.

XX

12-AUG-1996;

XX

96JP-00211805.

PR

18-SEP-1996;

XX

96JP-00246573.

XX

PA

(TAKE) TAKEDA CHEM IND LTD.

PA

WPI; 2000-452298/39.

XX

PA

Physiologically active polypeptide recognized as ligand by G protein-

PT

coupled receptor protein, for promoting secretion of oxytocin, as drugs

PT

for diseases relating to oxytocin secretion and in veterinary medicine.

XX

PS

Disclosure; Page 63; 72pp; Japanese.

XX

PS

Page 63; 72pp; Japanese.

XX

DR WPI; 2001-355552/37.
 PT Use of G protein receptor ligand or peptide for controlling corticotropin
 releasing hormone secretion.
 XX Disclosure; Page 75; 90pp; Japanese.

PS The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH) involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolism, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the invention

XX Sequence 21 AA;
 SQ ABU60847 standard; peptide; 21 AA.
 Query Match 87.8%; Score 72; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AWYASRGIRPVGVR 14
 ||||| ||||| |||||
 DB 7 AWYASRGIRPVGVR 19

RESULT 17
 AAW31396
 ID AAW31396 standard; peptide; 22 AA.
 XX AAW31396;
 AC AAW31396;
 XX 06-APR-1998 (first entry)
 DT Human type G protein-coupled receptor ligand fragment 6.
 DE XX
 KW G protein-coupled receptor; ligand; pharmaceutical; modulator;
 KW pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.
 OS Homo sapiens.
 XX PN WO9724436-A2.
 XX PD 10-JUL-1997.
 XX PF 26-DBC-1996; 96WO-JP003821.
 AC XX
 XX 06-MAY-2003 (first entry)
 DT XX
 DE Peptide production by gene recombination associated peptide #31.
 XX PR 28-DBC-1995; 95JP-00343371.
 KW PR 15-MAR-1996; 96JP-00059419.
 KW PR 12-AUG-1996; 96JP-00211805.
 KW PR 18-SEP-1996; 96JP-00246573.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Hinuma S, Habata Y, Kawamata Y, Hosoya M, Fujii R, Fukusumi S;
 XX PI Kitada C;
 XX DR WPI; 1997-363672/33.
 XX N-PSDB; AAV02433.
 PT Ligand peptide for G protein-coupled receptor - acts by modulating PT function in the central nervous system, pancreas and pituitary gland.
 XX Claim 2; Page 186; 258pp; English.

PS This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in AAW31396 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperprolactinaemia, hyperglycaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, anylotropic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the G protein-coupled receptor protein.

XX Sequence 22 AA;

PS The invention describes a method of producing a peptide comprising the excision of the N and C-termini of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide

Query Match	87.8%	Score 72;	DB 2;	Length 22;	AC AAG62536;
Best Local Similarity	100.0%	Pred. No. 1.0e-05;			XX 24-AUG-2001 (first entry)
Matches	13;	Conservative 0;	Mismatches 0;	Indels 0;	DE Human CRH releasing protein related peptide SEQ ID NO: 37.
					XX
Qy	2 AWYASRGIRPVGR 14				KW Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
Db	7 AWYASRGIRPVGR 19				KW analgesic; hyperaldosteronism; hypercortisolism; Addison's disease; adrenal gland hyperfunction; obesity.
RESULT 18					XX
AAB10367					OS Homo sapiens.
ID AAB10367 standard; peptide; 22 AA.					XX WO200135984-A1.
XX					XX
AC AAB10367;					PD 25-MAY-2001.
XX					XX
24-NOV-2000 (first entry)					PP 17-NOV-2000; 2000WO-JP008119.
XX					XX
DE Human oxytocin secretion promoting peptide SEQ ID NO: 37.					PR 18-NOV-1999; 99JP-00327900.
XX					PR 26-SEP-2000; 2000JP-00297073.
KW oxytocin secretion promoter; G protein-coupled receptor protein;					XX (TAKE) TAKEDA CHEM IND LTD.
KW treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;					PA
KW caesarean section; artificial fertilization; galactostasis; goat; pig;					XX
KW veterinary medicine; milk production.					PI Kitada C, Matsumoto H, Hinuma S;
XX					XX
OS Homo sapiens.					DR WPI; 2001-355552/37.
XX					XX
PN WO200038704-A1.					XX Use of G protein receptor ligand or peptide for controlling corticotropin
XX					PT releasing hormone secretion.
PD 06-JUL-2000.					XX Disclosure; Page 75; 90pp; Japanese.
XX					XX
PP 22-DEC-1999; 99WO-JP007199.					CC The present sequence describes a method of controlling the secretion of
XX					CC corticotrophin releasing hormone (CRH), involving the use of a G protein
PR 25-DEC-1998; 98JP-00369585.					CC receptor ligand. This can be used to control the secretion of CRH and is
XX					CC useful as an analgesic or for treating, preventing or ameliorating
PA (TAKE) TAKEDA CHEM IND LTD.					CC diseases associated with CRH secretion, such as hyperaldosteronism,
XX					CC hypercortisolism, secondary or chronic hypoadrenocorticism, Addison's
PI Matsumoto H, Kitada C, Hinuma S;					CC disease (including boredom, nausea, pigmentation, hypoadrenocorticism,
XX					CC hair loss, and hypotension), adrenal gland hypofunction and obesity. The
DR 2000-452298/39.					CC present sequence is a peptide used in the exemplification of the
XX					CC invention.
PT Physiologically-active polypeptide recognized as ligand by G protein-					XX Sequence 22 AA;
PT coupled receptor protein, for promoting secretion of oxytocin, as drugs					SQ
PT for diseases relating to oxytocin secretion and in veterinary medicine.					Query Match 87.8%; Score 72; DB 4; Length 22;
XX					Best Local Similarity 100.0%; Pred. No. 1.6e-05;
PS Disclosure; Page 64; 72pp; Japanese.					Mismatches 0; Indels 0; Gaps 0;
XX					AC ABU60848; peptide; 22 AA.
CC This invention describes a novel oxytocin secretion-regulating agent					RESULT 20
CC which contains a ligand peptide or its salt for the G protein-coupled					ABU60848
CC receptor protein. It is useful in the form of drugs for ameliorating,					XX 06-MAY-2003 (first entry)
CC preventing and treating diseases relating to oxytocin secretion e.g. weak					DT DT
CC pains and atonic bleeding, before and after expulsion of placenta,					XX Peptide production by gene recombination associated peptide #32.
CC uterine recovery failure, caesarean section, stoppage of artificial					DB DB
CC fertilization or galactostasis and is also applicable in veterinary					XX Peptide production; low-molecular peptide; Kiss-1; GPR8 ligand;
CC medicine for promoting milk production in cow, goat and pig. This					KW KW
CC sequence represents a human peptide which acts as an oxytocin secretion					XX gene recombination.
XX promoter					OS Homo sapiens.
SQ Sequence 22 AA;					XX WO0029829-A1.
Query Match 87.8%; Score 72; DB 3; Length 22;					XX
Best Local Similarity 100.0%; Pred. No. 1.6e-05;					PN WO0029829-A1.
Matches 13;					XX
Conservative 0;					PD 21-NOV-2002.
Mismatches 0;					XX
Indels 0;					
Qy 2 AWYASRGIRPVGR 14					
Db 7 AWYASRGIRPVGR 19					
RESULT 19					
AAG62536					
ID AAG62536 standard; peptide; 22 AA.					
XX					

CC growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglycidaemia, hyperprolactinaemia, hypertension, Turner's syndrome, neurosis, asthma, cancer, panicattack, renal disease, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amyotrophic lateral sclerosis, acute myocardial infarction, interictus, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assay can also be developed to screen compounds which are capable of altering the binding activity of the G protein-coupled receptor protein

XX ligand affecting activation of the G protein-coupled receptor protein

Sequence 31 AA;

Query Match AAW87615 standard; peptide; 31 AA.

Best Local Similarity 100.0%; Pred. No. 2.4e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14

Db 18 AWYASRGIRPVGR 30

RESULT 23

AAW87615

ID AAW87615

XX

AC AAW87615;

XX

DT 29-MAR-1999 (first entry)

XX

DE Human 19P2 ligand.

XX

KW 19P2 ligand; G protein coupled receptor; pituitary;

XX prolactin releasing peptide; human; dementia; breast cancer; therapy.

XX

OS Homo sapiens.

XX

EP887417-A2.

XX

PD 30-DEC-1998.

XX

PP 25-JUN-1998;

XX

PR 27-JUN-1997;

XX

PA (TAKE) TAKEDA CHEM IND LTD.

PI

Moriya T, Tanaka Y, Nishimura O;

XX

WPI; 1999-047884/05.

XX

This is the amino acid sequence of the human pituitary G protein-coupled receptor ligand 19P2L. A method suitable for commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see AAV83796-97) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation followed by ammonolysis. 19P2L has prolactin secretion-stimulating and (at high doses) prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including: senile dementia, cerebrovascular dementia, and dementia associated with genealogical disorders (e.g. Alzheimer's disease, Parkinson's disease, Pick's disease, Huntington's disease, infectious diseases (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or toxicosis (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism, intoxication by drugs, metal and organic compounds) tumourigenic diseases (e.g. brain tumour), traumatic diseases (e.g. chronic subarachnoidal hemorrhage, and other types of dementia, depression, hyperactive child syndrome

CC (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hypo-CC and hypersecretion respectively, including: hyperprolactinaemia, CC pituitary adenoma, breast cancer, infertility, impotence and autoimmune disease (hypersecretion disorders), and seminal vesicle hypoplasia, CC osteoporosis, menopausal syndrome and renal failure (hyposecretion CC disorders). The 19P2 polypeptide/amide is also useful as a test reagent CC for study of the prolactin secretory function or as a lactogogue in CC mammalian farm animals

XX Sequence 31 AA;

Query Match AAW97235 standard; peptide; 31 AA.

Best Local Similarity 100.0%; Pred. No. 2.4e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14

Db 18 AWYASRGIRPVGR 30

RESULT 24

AAW97235

ID AAW97235

XX

AC AAW97235;

XX

DT 06-MAY-1999 (first entry)

XX

DE Human type ligand polypeptide fragment.

XX

KW Rat type ligand; modulation; prolactin secretion; gonecyst cacogenesis;

XX G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation;

XX pituitary adenomatosis; brain tumour; emmenopathy; autoimmune disease;

XX prolactinoma; infertility; amenorrhea; galactorrhea;

XX acromegaly; Chiari-Erbomel syndrome; Argonz-del Castillo syndrome;

XX Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;

XX contraceptive; placental function; choriocarcinoma; hydatid mole;

XX interruption mole; abortion; unthrifly fetus; abnormal saccharometabolism;

XX abnormal lipidmetabolism; oxytocia.

XX

OS Homo sapiens.

XX

PN WO9858962-A1.

XX

PD 30-DEC-1998.

XX

PP 22-JUN-1998;

XX

PR 23-JUN-1997;

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PD 30-DEC-1998.

XX

PI Hinuma S, Kawamata Y, Fujii R, Matsumoto H;

XX

WPI; 1999-105614/09.

XX

DR 9880-JP002765.

XX

PR 975P-00165437.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

Claim 3; Page 159; 241pp; English.

XX

CC The present sequence represents a human type ligand fragment. It is used

CC in the course of the invention. The specification describes an agent for

CC modulating prolactin secretion which comprises a ligand polypeptide or a

CC salt, for a G protein-coupled receptor (GPR) protein. The agents for

CC promoting prolactin secretion can be used for treating or preventing

CC tumours, autoimmune disease or abnormal pregnancy.

XX

CC

DE Prolactin releasing peptide SEQ ID NO:165.
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX OS Homo sapiens.
 OS Synthetic.
 PN WO20069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000;
 XX
 PR 17-MAY-1999;
 PR 99US-0134406P.
 PR 10-SEP-1999;
 PR 99US-0153406P.
 PR 15-OCT-1999;
 PR 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 Disclosure: Page 244; 733pp; English.
 XX
 The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxylthiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC They are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB9029 to AAB2441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 Sequence 31 AA;
 Query Match 87.8%; Score 72; DB 4; Length 31;
 Best Local Similarity 100%; Pred. No. 2.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 29
 AAG62531
 ID AAG62531 standard; peptide; 31 AA.
 XX
 AC AAG62531;
 AC
 XX
 DT 24-AUG-2001 (First entry)
 XX
 DE Human CRH releasing protein related peptide SEQ ID NO: 32.
 XX
 ID AAG62531
 XX
 KW Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
 KW analgesic; hyperalgesic; hypercortisolism; hypoadrenocorticism;
 KW Addison's disease; adrenal gland hyperfunction; obesity.
 XX
 OS Homo sapiens.
 XX
 PN WO200135384-A1.
 XX
 DE Prolactin releasing peptide SEQ ID NO:169.
 XX
 AC AAB90995;
 AC
 XX
 DT 22-JUN-2001 (First entry)
 XX
 DE Prolactin releasing peptide; peptide; conjugation;
 XX
 KW Protection; endogenous therapeutic peptide; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 PN WO200135384-A1.
 XX
 DE AAB90995
 AC AAB90995;
 AC
 XX
 DT 25-MAY-2001.
 XX

PF 17-NOV-2000; 2000WO-JP008119.
 PR 18-NOV-1999; 99JP-00327900.
 PR 26-SEP-2000; 2000JP-00297073.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Kitada C, Matsumoto H, Hinuma S;
 DR; WPI; 2001-355552/37.
 XX Use of G protein receptor ligand or peptide for controlling corticotropin
 PT releasing hormone secretion.
 XX Claim 3; Page 73-74; 90pp; Japanese.
 CC The present sequence describes a method of controlling the secretion of
 CC corticotrophin releasing hormone (CRH), involving the use of a G protein
 CC receptor ligand. This can be used to control the secretion of CRH and is
 CC useful as an analgesic or for treating, preventing or ameliorating
 CC diseases associated with CRH secretion such as hyperaldosteronism,
 CC hypercortisolæmia, secondary or chronic hypoadrenocorticism, Addison's
 CC disease (including boredom, nausea, pigmentation, hypogonadism, hair
 CC loss, and hypertension), adrenal gland hypofunction and obesity. The
 CC present sequence is a peptide used in the exemplification of the
 CC invention
 SQ Sequence 31 AA;

Query Match 87.8%; Score 72; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

RESULT 31
 ABU60843 standard; peptide; 31 AA.
 ID ABU60843
 XX
 AC ABU60843;
 XX DT 06-MAY-2003 (first entry)
 XX Peptide production by gene recombination associated peptide #27.
 DE XX
 XX Peptide production; low-molecular peptide; Kiss-1; GPR8 ligand;
 KW XX
 KW Gene recombination.
 KW XX
 KW Homo sapiens.
 OS XX
 PN WO200292529-A1.
 XX
 XX DT 21-NOV-2002.
 XX
 XX
 AC AAE26401;
 XX
 XX 13-DEC-2002 (first entry)
 XX
 DE Human P_rRP-31 peptide.
 KW XX
 KW Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;
 KW PRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
 KW insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
 KW anticonvulsant.
 OS XX
 Homo sapiens.
 PN US2002037533-A1.
 XX
 PD 28-MAR-2002.
 XX
 PR 17-AUG-2001; 2001US-00932161.
 XX
 PR 28-APR-2000; 2000US-00560915.
 XX
 (CIVELLI) CIVELLI O.
 PA (LINS) LIN S.
 XX
 PI Civelli O, Lin S;
 DR
 DR; WPI; 2002-433931/43.
 XX
 Screening for compounds useful for promoting wakefulness or sleep, and
 PR for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
 PR apnea, comprises administering a prolactin releasing peptide agonist or

PT antagonist.
 XX Disclosure; Page 24; 35pp; English.
 PS
 XX
 CC The present invention relates to a method of screening for compounds for
 CC promoting wakefulness or sleep in a mammal. The method involves
 CC administering a prolactin releasing peptide (PRP) receptor (GPR10)
 CC agonist or antagonist respectively and determining the ability of the
 CC compound to promote wakefulness or sleep. The compounds identified from
 CC the method are used in the therapy of epilepsy and other diseases
 CC associated with absence seizures and in promoting wakefulness and sleep
 CC in individuals having sleep disorders such as insomnia and narcolepsy.
 CC PRP receptor agonists may be used to treat common disorders which lead
 CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and
 CC psychogenic hypersomnia. PRP receptor antagonists are useful for
 CC promoting sleep and for treating insomnia such as adjustment sleep
 CC disorder and psychophysiological insomnia. The present sequence is human
 CC PRP-31 peptide.
 XX Sequence 31 AA;
 SQ
 Query Match 87.8%; Score 72; DB 5; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 2 AWYASRGIRGPVGR 14
 ||||| ||||| |||||
 Db 18 AWYASRGIRGPVGR 30
 ||||| ||||| |||||
 ||||| |||||

Query Match 87.8%; Score 72; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

RESULT 30
 AAE26401 standard; peptide; 31 AA.
 ID AAE26401
 XX
 AC AAE26401;
 XX DT 06-MAY-2003 (first entry)
 XX
 DE Peptide production by gene recombination associated peptide #27.
 KW XX
 KW Peptide production; low-molecular peptide; Kiss-1; GPR8 ligand;
 KW XX
 KW Gene recombination.
 KW XX
 KW Homo sapiens.
 OS XX
 PN WO200292529-A1.
 XX
 XX DT 21-NOV-2002.
 XX
 XX
 AC AAE26401;
 XX
 XX 13-DEC-2002 (first entry)
 XX
 DE Human P_rRP-31 peptide.
 KW XX
 KW Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;
 KW PRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
 KW insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
 KW anticonvulsant.
 OS XX
 Homo sapiens.
 PN US2002037533-A1.
 XX
 PD 28-MAR-2002.
 XX
 PR 17-AUG-2001; 2001US-00932161.
 XX
 PR 28-APR-2000; 2000US-00560915.
 XX
 (CIVELLI) CIVELLI O.
 PA (LINS) LIN S.
 XX
 PI Civelli O, Lin S;
 DR
 DR; WPI; 2002-433931/43.
 XX
 Screening for compounds useful for promoting wakefulness or sleep, and
 PR for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
 PR apnea, comprises administering a prolactin releasing peptide agonist or

PT antagonist.
 XX Disclosure; Page 24; 35pp; English.
 PS
 XX
 CC The present invention describes a method of producing a peptide comprising the
 CC N and C-termini of a target peptide with enzymes or
 CC chemically through the attached cleavage sites repeated by ligation in a
 CC precursor protein. The method is for producing (low-molecular) peptides
 CC e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the
 CC gene recombination technique through tandem repeats to provide a
 CC precursor protein with specific cleavage sites. With this method, peptide
 CC production can be carried out easily to provide large quantities of the

CC required peptides. This is the amino acid sequence of a peptide
CC associated with the peptide production method of the invention
XX

SQ Sequence 31 AA;

Query Match 87.8%; Score 72; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AWYASRGIRPVGR 14

Db 18 AWYASRGIRPVGR 30

RESULT 32

ABU60827 ABU60827 standard; peptide; 31 AA.

XX

AC ABU60827;

XX

DT 06-MAY-2003 (first entry)

XX

DE Peptide production by gene recombination associated peptide #11.

XX

DE Peptide production; low-molecular peptide; Kiss-1; GPR8 ligand;

XX

DE Gene recombination.

XX

OS Homo sapiens.

XX

PN WO200292829-A1.

XX

PD 21-NOV-2002.

XX

PP 16-MAY-2002; 2002WO-JP004735.

XX

PP 17-MAY-2001; 2001JP-00147341.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Nishimura O, Suegaga M, Ito T, Kitada C;

XX

DR WPI; 2003-129305/12.

XX

PT Process for producing peptides e.g. Kiss-1 peptide and GPR8 ligand for
subsequent applications by gene recombination technique through tandem
repeats to provide precursor protein with specific cleavage sites.

XX

PS Disclosure; Page 59; 87pp. Japanese.

XX

CC The invention describes a method of producing a peptide comprising the
CC N and C terminals of a target peptide with enzymes or
CC chemically through the attached cleavage sites repeated by ligation in a
CC precursor protein. The method is for producing (low-molecular) peptides
CC e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the
CC gene recombination technique through tandem repeats to provide a
CC precursor protein with specific cleavage sites. With this method, peptide
CC production can be carried out easily to provide large quantities of the
CC required peptides. This is the amino acid sequence of a peptide
CC associated with the peptide production method of the invention

XX

SQ Sequence 31 AA;

Query Match 87.8%; Score 72; DB 6; Length 31;

Best Local Similarity 100.0%; Pred. No. 2.4e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AWYASRGIRPVGR 14

Db 18 AWYASRGIRPVGR 30

RESULT 33

ADCC71228

ID ADC71228 standard; peptide; 31 AA.

XX

AC ADC71228;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human peptide sequence 2 related to the human serine protease;
KW human; serine protease precursor; hormone; neurohypophysial; diabetes;
KW diabetic retinopathy; cataract; antidiabetic; ophthalmological.

XX

OS Homo sapiens.

XX

PN WO2003062429-A1.

XX

PD 31-JUL-2003.

XX

PP 2003WO-JP000547.

XX

PR 22-JAN-2003; 2003WO-JP000547.

XX

PR 23-JAN-2002; 2002JP-00013449.

XX

PR 10-OCT-2002; 2002JP-00298003.

XX

PA (YAMA) YAMANOUCHI PHARM CO LTD.

XX

PI Kagoshima M, Yamaji N, Takeda M, Abe K, Kawabe T;

XX

DR WPI; 2003-598754/56.

XX

PT Peptidase precursor for developing treatment for diabetes and cataracts.

XX

PS Example 10; SEQ ID NO 13; 61pp; Japanese.

XX

CC This invention relates to a novel human serine protease precursor
CC polypeptide. Specifically, it refers to a novel type II transmembrane
CC serine protease that participates in the control of hormones produced by
CC the pancreatic gland. As such, it can be used in a screening method for
CC the identification of compounds that are useful for the treatment of
CC diseases where a neurohypophysial hormone participates, such as
CC diabetes, diabetic retinopathy and cataract. The present invention
CC describes the compounds of this invention as antidiabetic and
CC ophthalmological. This peptide sequence is human peptide 2 related to the
CC human serine protease of the invention.

XX

SQ Sequence 31 AA;

Query Match 87.8%; Score 72; DB 7; Length 31;

Best Local Similarity 100.0%; Pred. No. 2.4e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AWYASRGIRPVGR 14

Db 18 AWYASRGIRPVGR 30

RESULT 34

AAW31392 standard; peptide; 32 AA.

XX

AC AAW31392;

XX

DT 06-APR-1998 (first entry)

XX

DE Human type G protein-coupled receptor ligand fragment 2.

XX

KW G protein-coupled receptor; ligand binding; pharmaceutical; modulator;

XX

OS Homo sapiens.

XX

PN WO9724436-A2.

XX

PD 10-JUL-1997.

Db 18 AWYASRGIRPVGR 30

RESULT 39

ABB10364 standard; peptide; 33 AA.

XX

AC AAB10364;

XX

DT 24-NOV-2000 (First entry)

XX

DE Human oxytocin secretion promoting peptide SEQ ID NO: 34.

XX

KW Human oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; Pig; veterinary medicine; milk production.

XX

OS Homo sapiens.

XX

PN WO200038704-A1.

XX

PD 06-JUL-2000.

XX

PP 22-DEC-1999; 99W0-JP007199.

XX

PR 25-DEC-1998; 98JP-00369585.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PT Matsumoto H, Kitada C, Hinuma S;

DR WPI; 2000-452298/39.

XX

PT Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.

XX

PS Disclosure; Page 62-63; 72pp; Japanese.

XX

CC This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion promoter.

XX

SQ Sequence 33 AA;

Query Match 87.8%; Score 72; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.5e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AWYASRGIRPVGR 14

||| ||| ||| |||

Db 18 AWYASRGIRPVGR 30

Search completed: February 25, 2004, 06:42:35

Job time : 55 secs

XX

RESULT 40

ARG62533

ID ARG62533 standard; peptide; 33 AA.

XX

AC ARG62533;

XX

DT 24-AUG-2001 (First entry)

XX

DE Human CRH releasing protein related peptide SEQ ID NO: 34.

KW Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;

LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 93:
 US-09-776-971-93

Query Match 93.9%; Score 77; DB 3; Length 15;
 Best Local Similarity 92.9%; Pred. No. 1.2e-06; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 1;

Qy 1 CAWYASRGIRPVGR 14
 Db 1 CAWZAGRGRIPRVGR 14

RESULT 2
 US-09-105-678A-46
 Sequence 46, Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Shigenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION NUMBER:
 APPLICATION NUMBER: US/09/105.678A
 FILING DATE: 26-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-09-105-678A-46

Query Match 87.8%; Score 72; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 4
 US-09-421-208-46
 Sequence 46, Application US/09421208
 Patent No. 6258561
 GENERAL INFORMATION:
 APPLICANT: Shunaga, Masato

RESULT 3

APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-421-208-46

Query Match 87.8%; Score 72; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 5
 US-09-560-915-1B
 ; Sequence 1.8, Application US/09560915
 ; Patent No. 6383764
 ; GENERAL INFORMATION:
 ; APPLICANT: Civelli, Olivier
 ; APPLICANT: Lin, Steven
 ; TITLE OF INVENTION: Therapeutic Compositions and Methods
 ; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
 ; FILE REFERENCE: P-DC 3534
 ; CURRENT APPLICATION NUMBER: US/09/560,915
 ; CURRENT FILING DATE: 2000-05-28
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-560-915-1B

Query Match 87.8%; Score 72; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 6
 US-09-105-678A-47
 ; Sequence 47, Application US/09105678A
 ; Patent No. 6103842
 ; GENERAL INFORMATION:
 ; APPLICANT: Sueenga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/105,678A
 ; FILING DATE: 26-JUN-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 172118/1997
 ; FILING DATE: 27-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conlin, David G.
 ; REGISTRATION NUMBER: 27,026
 ; APPLICATION NUMBER: JP 172118/1997
 ; FILING DATE: 27-JUN-1997
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; INFORMATION FOR SEQ ID NO: 46:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-105-678A-47

Query Match 87.8%; Score 72; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 7
 US-08-776-971-65
 ; Sequence 65, Application US/08776971B
 ; Patent No. 6228984
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinuma, Shuji
 ; APPLICANT: Habata, Yugo
 ; APPLICANT: Kawamata, Yuji
 ; APPLICANT: Hosoya, Masaki
 ; APPLICANT: Fujii, Ryō
 ; APPLICANT: Fukusumi, Shōji
 ; APPLICANT: Kiteda, Chieko
 ; TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE

NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disquette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1996
 APPLICATION NUMBER: JP 7/3433371
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 65:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 65:
 -08-776-971-65
 Query Match 87.8% Score 72; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0
 2 AWYASRGIRYGR 14
 ||||| |||||
 7 AWYASRGIRYGR 19
 -09-421-208-47
 Sequence 47, Application US/09421208
 GENERAL INFORMATION:
 APPLICANT: Sunaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA

TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-105-678A-48

Query Match 87.8%; Score 72; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 11
 US-09-421-208-48
 ; Sequence 48, Application US/09421208
 ; Patent No. 625851

; GENERAL INFORMATION:
 ; APPLICANT: Sueenaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/421,208
 ; FILING DATE:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/105,678
 ; FILING DATE: 26-JUN-1998
 ; APPLICATION NUMBER: JP 172118/1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conlin, David G.
 ; REGISTRATION NUMBER: 27,026
 ; REFERENCE/DOCKET NUMBER: 48466-342
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; INFORMATION FOR SEQ ID NO: 48:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 22 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-09-421-208-48

Query Match 87.8%; Score 72; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 12
 US-09-105-678A-9
 ; Sequence 9, Application US/09105678A

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 61:

US-08-776-71-61

Query Match 87.8%; Score 72; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 18 AWYASRGIRPVGR 30

RESULT 15

US-09-421-208-9

Sequence 9, Application US/09421208

Patent No. 6258561

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

APPLICATION NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

FILING DATE: 27-JUN-1997

APPLICATION NUMBER: US/09/421,208

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

APPLICATION NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-421-208-9

Query Match 87.8%; Score 72; DB 3; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

RESULT 16

US-09-421-208-43

Sequence 43, Application US/09421208

Patent No. 6258561

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

APPLICATION NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-421-208-43

Query Match 87.8%; Score 72; DB 3; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

RESULT 17

US-09-566-915-15

Sequence 15, Application US/09560915

Patent No. 6383764

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

```

TITLE OF INVENTION: Therapeutic Compositions and Methods
; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/09/560,915
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-560-915-15

Query Match 87.8%; Score 72; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; G
; 2 AMYASRGIRPVGR 14
; 18 AMYASRGIRPVGR 30

Qy
Db

RESULT 18
US-09-105-678A-44
; Sequence 44, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Sueenga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,678A
; FILING DATE: 26-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 4B466-342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3700
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-44

Query Match 87.8%; Score 72; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; G
; 2 AMYASRGIRPVGR 14
; 18 AMYASRGIRPVGR 30

```

RESULT 1.9
 US-08-776-971-62
 i Sequence 62, Application US/0
 i Patent No. 622894
 i GENERAL INFORMATION:
 i i APPLICANT: Hinuma, Shu
 i i Habata, Yugo
 i i Kawamata, Yasu
 i i Hosoya, Mas
 i i Fujii, Ryo
 i i Fukusumi, S
 i i Katada, Chi
 i i TITLE OF INVENTION: PO
 i i NUMBER OF SEQUENCES: 1
 i i CORRESPONDENCE ADDRESS:
 i i ADDRESSEE: DIKE,
 i i STREET: 130 Water
 i i CITY: Boston
 i i STATE: MA
 i i COUNTRY: USA
 i i ZIP: 02109
 i i COMPUTER READABLE FORM
 i i MEDIUM TYPE: Disk
 i i COMPUTER: IBM com
 i i OPERATING SYSTEM:
 i i SOFTWARE: FastSeq
 i i CURRENT APPLICATION DATA
 i i APPLICATION NUMBER:
 i i FILING DATE: 06-F
 i i CLASSIFICATION: <
 i i PRIOR APPLICATION DATA
 i i APPLICATION NUMBER:
 i i FILING DATE: 28-D
 i i APPLICATION NUMBER:
 i i FILING DATE: 28-D
 i i APPLICATION NUMBER:
 i i FILING DATE: 15-M
 i i APPLICATION NUMBER:
 i i FILING DATE: 12-A
 i i APPLICATION NUMBER:
 i i FILING DATE: 18-S
 i i ATTORNEY/AGENT INFORMATION:
 i i NAME: Conlin, Dav
 i i REGISTRATION NUMBER:
 i i REFERENCE/DOCKET:
 i i TELECOMMUNICATION INFO:
 i i TELEPHONE: 617-522-
 i i TELEFAX: 617-523-
 i i INFORMATION FOR SEQ ID NO:
 i i SEQUENCE CHARACTERISTICS:
 i i LENGTH: 32 amino
 i i TYPE: amino acid
 i i STRANDEDNESS: sin
 i i TOPOLOGY: linear
 i i MOLECULE TYPE: protein
 i i FRAGMENT TYPE: interna
 i i SEQUENCE DESCRIPTION:
 i i US-08-776-971-62
 Query Match 87.8%
 Best Local Similarity 100.0
 Matches 13; Conservative
 QY 2 AWYASRGIRPVGR 14
 DO 18 AWYASRGIRPVGR 30
 RESULT 20
 REC 08-11-2014 44

Sequence 44, Application US/09421208
 Patent No 6255561
 GENERAL INFORMATION:
 APPLICANT: Suenga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIME, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-421-208-44

Query Match 87.8%; Score 72; DB 3; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 21
 US-09-105-678A-45
 Sequence 45, Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Suenga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIME, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-45

Query Match 87.8%; Score 72; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 22
 US-09-776-971-63
 Sequence 63, Application US/08776971B
 Patent No. 6228944
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 Habata, Yugo
 Kawamat, Yuji
 Hosoya, Masaki
 Fujii, Ryo
 Fukusumi, Shoji
 Kitada, Chieko
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIME, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1996
 APPLICATION NUMBER: JP 7/343371
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 16-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6410
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 63:
 US-08-776-971-63

Query Match 87.8%; Score 72; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 24
 US-08-776-971-59

Query Match 87.8%; Score 72; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 23
 US-08-421-208-45

Query Match 87.8%; Score 72; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 23
 US-08-421-208-15

Query Match 87.8%; Score 72; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 140

CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASCAL FOR Windows Version 2.0

APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1996
 APPLICATION NUMBER: JP 7/343371
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 87 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:
 US-08-776-971-59

Query Match 87.8%; Score 72; DB 3; Length 87;

Best Local Similarity 100.0%; Pred. No. 5.2e-05; Mismatches 0; Indels 0; Gaps 0; Db 40 AWYASRGIRPVGR 52

Qy 2 AWYASRGIRPVGR 14
Db 40 AWYASRGIRPVGR 52

RESULT 25
US-08-776-971-135
Sequence 135, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/03821
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 7/343371
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/03821
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/244573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 135:
US-08-776-971-135

Query Match 87.8%; Score 72; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Mismatches 0; Indels 0; Gaps 0; Db 40 AWYASRGIRPVGR 52

Qy 2 AWYASRGIRPVGR 14
Db 40 AWYASRGIRPVGR 52

RESULT 27
US-09-105-678A-30

Sequence 30, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSQL for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 41176

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-08-776,971-4

Query Match 82.9%; Score 68; DB 3; Length 19;

Best Local Similarity 92.3%; Pred. No. 5e-05; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14

Db 7 AWYAGRGIRPVGR 19

RESULT 29

US-09-421-208-3-0

Sequence 30, Application US/09421208

Patent No. 6258561

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

ZIP: 02109

COMPUTER READABLE FORM:

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208

FILING DATE:

RESULT 28

US-08-776,971-4

Sequence 4, Application US/08776971B

GENERAL INFORMATION:

Patent No. 6228984

APPLICANT: Hinuma, Shuji

Habata, Yugo

Kawamata, Yuji

Hosoya, Masaki

Fujii, Ryo

Fukusumi, Shoji

Kitada, Chieko

TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE

NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-09-105-678A-34
 Query Match 82.9%; Score 68; DB 3; Length 19;
 Best Local Similarity 92.3%; Pred. No. 5e-05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASGRGPVGR 14
 Db 7 AWYAGRGPVGR 19

RESULT 31
 US-08-776-971-8
 Sequence 8, Application US/08776971B
 Patent No. 622884
 GENERAL INFORMATION:
 APPLICANT: Hiruma, Shuji
 Habata, Yugo
 Kawamata, Yuji
 Hosoya, Masaki
 Fujisumi, Shoji
 Kitada, Chieko
 TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1996
 APPLICATION NUMBER: JP 7/343371:
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: JP 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-08-776-971-8

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678A
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

RESULT 32
 US-08-776-971-8
 Sequence 8, Application US/08776971B
 Patent No. 622884
 GENERAL INFORMATION:
 APPLICANT: Hiruma, Shuji
 Habata, Yugo
 Kawamata, Yuji
 Hosoya, Masaki
 Fujisumi, Shoji
 Kitada, Chieko
 TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1996
 APPLICATION NUMBER: JP 7/343371:
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: JP 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-08-776-971-8

Qy 2 AWYASRGIRPVYGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 32
 US-08-776-971-98
 / Sequence 98, Application US/08776971B
 / Patent No. 6228984
 / GENERAL INFORMATION:
 / APPLICANT: Hiruma, Shuji
 Habata, Yugo
 Kawamata, Yuji
 Hosoya, Masaki
 Fujii, Ryo
 Fukushima, Shoji
 Kitada, Chieko
 TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ For Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1996
 APPLICATION NUMBER: JP 7/3433171
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 98:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 98:
 US-08-776-971-98
 Query Match 82.9%; Score 68; DB 3; Length 20;
 Best Local Similarity 92.3%; Pred. No. 5.0e-05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVYGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 34
 US-09-421-208-34
 / Sequence 34, Application US/09421208
 / Patent No. 6258561
 / GENERAL INFORMATION:
 / APPLICANT: Sueyaga, Masato
 / APPLICANT: Moriya, Takeo
 / APPLICANT: Taraka, Yoko
 / APPLICANT: Niishimura, Osamu
 / TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 / NUMBER OF SEQUENCES: 52
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 / STREET: 130 Water Street
 / CITY: Boston
 / STATE: MA
 / COUNTRY: USA
 / ZIP: 02109
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/421-208
 / FILING DATE:
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 09/105,678
 / FILING DATE: 26-JUN-1998
 / APPLICATION NUMBER: JP 172118/1997
 / FILING DATE: 27-JUN-1997
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Conlin, David G.
 / REGISTRATION NUMBER: 27,026
 / REFERENCE/DOCKET NUMBER: 48466-342
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 617-523-3410
 / TELEFAX: 617-523-6440
 / INFORMATION FOR SEQ ID NO: 34:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 20 amino acids
 / TYPE: amino acid
 / STRANDEDNESS:
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide
 US-09-421-208-34
 Query Match 82.9%; Score 68; DB 3; Length 20;
 Best Local Similarity 92.3%; Pred. No. 5.3e-05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 34
 US-09-560-915-16
 / Sequence 16, Application US/09560915
 / Patent No. 6383764
 / GENERAL INFORMATION:
 / APPLICANT: Civelli, Olivier
 / APPLICANT: Lin, Steven
 / TITLE OF INVENTION: Therapeutic Compositions and Methods
 / Relating To Prolactin Releasing Peptide (PrRP)
 / FILE REFERENCE: P-UC 3534
 / CURRENT APPLICATION NUMBER: US/09/560,915
 / CURRENT FILING DATE: 2000-04-28
 / NUMBER OF SEQ ID NOS: 24
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 16
 / LENGTH: 20
 / TYPE: PRT
 / ORGANISM: Bos taurus
 /

RESULT 33

US-09-560-915-16

Query Match 82.9%; Score 68; DB 4; Length 20;
 Best Local Similarity 92.3%; Pred. No. 5.3e-05; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1;

Qy 2 AWYASRGIRPVGR 14

Db 7 AWYAGRGIRPVGR 19

RESULT 35
 US-09-105-678A-35
 Sequence 35, Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105, 678A
 FILING DATE: 26-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 1-72118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Corlin, David G.
 REGISTRATION NUMBER: 27, 026
 REFERENCE DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-35

Query Match 82.9%; Score 68; DB 3; Length 21;
 Best Local Similarity 92.3%; Pred. No. 5.5e-05; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1;

RESULT 37
 US-09-421-208-35
 Sequence 35, Application US/09421208
 Patent No. 6358561
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYAGRGIRPVGR 19

RESULT 36
 US-08-776-971-9
 Sequence 9, Application US/08776971B
 Patent No. 622894
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 Habata, Yugo
 Kawamata, Yuji

STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 MOLECULE TYPE: peptide
 US-09-105-678A-36

Query Match 82.9%; Score 68; DB 3; Length 21;
 Best Local Similarity 92.3%; Pred. No. 5.5e-05; Indels 0; Gaps 0;
 Matches 12; Conservative 1; Mismatches 0; NMatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYAGRGIRPVGR 19

RESULT 39
 US-08-776-971-10

Query Match 82.9%; Score 68; DB 3; Length 21;
 Best Local Similarity 92.3%; Pred. No. 5.8e-05; Indels 0; Gaps 0;
 Matches 12; Conservative 1; Mismatches 0; NMatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYAGRGIRPVGR 19

RESULT 39
 US-08-776-971-10

Query Match 82.9%; Score 68; DB 3; Length 21;
 Best Local Similarity 92.3%; Pred. No. 5.5e-05; Indels 0; Gaps 0;
 Matches 12; Conservative 1; Mismatches 0; NMatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYAGRGIRPVGR 19

RESULT 38
 US-09-105-678A-36

Sequence 36: Application US/09105678A
 Patent No. 6103842
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 FRAGMENT TYPE: internal
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-776-971-10

Query Match 82.9%; Score 68; DB 3; Length 22;
 Best Local Similarity 92.3%; Pred. No. 5.8e-05; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AWYASRGIRGPYGR 14
 Db 7 AWYAGRGRGPYGR 19

RESULT 40
 US-09-421-208-36
 Sequence 36, Application US/09421208
 Patent No. 6258561

GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172116/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-3442
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Query Match 82.9%; Score 68; DB 3; Length 22;
 Best Local Similarity 92.3%; Pred. No. 5.8e-05; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AWYASRGIRGPYGR 14
 Db 7 AWYAGRGRGPYGR 19



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	21	68	82.9	98	13
	22	68	82.9	98	13
	23	64	78.0	20	13
	24	64	78.0	20	13
	25	64	78.0	20	14
	26	64	78.0	31	9
	27	64	78.0	31	13
	28	64	78.0	31	13
	29	64	78.0	31	14
	30	64	78.0	70	13
	31	64	78.0	82	13
	32	64	78.0	86	13
	33	64	78.0	91	13
	34	63	76.8	29	13
	35	53	64.6	25	13
	36	46	56.1	647	15
	37	44	53.7	411	15
	38	44	53.7	555	15
	39	43	52.4	402	14
	40	43	52.4	592	14
	41	43	52.4	838	14
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	43	42	51.2	288	14
	44	42	51.2	645	10
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string table:	BLOSUM62				
	Gapext 10.0 , Gapext 0.5				
searched:	809742 seqs, 211153299 residues				
	all number of hits satisfying chosen parameters:	809742			
	maximum DB seq length: 0				
	maximum DB seq length: 2000000000				
post-processing:	Minimum Match 0%				
	Maximum Match 100%				
	Listing First 45 summaries				
	Published Applications AA:*				

ט'ז נסחנות

SUMMARIES									
Query	Match	Length	DB	ID	Description				
5: /cgn2_6_ptodata/1/pubpaas/us07_new_pub..pep:*	72	87.8	20	9	US-09-932-161-18	Sequence 18, Appl			
6: /cgn2_6_ptodata/1/pubpaas/pcutcs_pubcomb..pep:*	72	87.8	20	14	US-10-096-77-18	Sequence 18, Appl			
7: /cgn2_6_ptodata/1/pubpaas/us08_new_pub..pep:*	72	87.8	31	9	US-09-932-161-15	Sequence 15, Appl			
8: /cgn2_6_ptodata/1/pubpaas/us08_pubcomb..pep:*	72	87.8	31	14	US-10-096-77-15	Sequence 15, Appl			
9: /cgn2_6_ptodata/1/pubpaas/us09_pubcomb..pep:*	72	87.8	87	13	US-10-044-992-92	Sequence 92, Appl			
10: /cgn2_6_ptodata/1/pubpaas/us09b_pubcomb..pep:*	72	82.9	19	13	US-10-044-992-27	Sequence 27, Appl			
11: /cgn2_6_ptodata/1/pubpaas/us09c_pubcomb..pep:*	72	82.9	19	20	US-09-932-161-16	Sequence 16, Appl			
12: /cgn2_6_ptodata/1/pubpaas/us09_new_pub..pep:*	72	87.8	20	14	US-10-044-992-42	Sequence 42, Appl			
13: /cgn2_6_ptodata/1/pubpaas/us10a_pubcomb..pep:*	72	87.8	31	9	US-10-096-77-15	Sequence 16, Appl			
14: /cgn2_6_ptodata/1/pubpaas/us10b_pubcomb..pep:*	72	87.8	31	14	US-10-044-992-44	Sequence 43, Appl			
15: /cgn2_6_ptodata/1/pubpaas/us10c_pubcomb..pep:*	72	87.8	87	13	US-09-932-161-13	Sequence 44, Appl			
16: /cgn2_6_ptodata/1/pubpaas/us10_new_pub..pep:*	72	82.9	31	13	US-10-044-992-39	Sequence 13, Appl			
17: /cgn2_6_ptodata/1/pubpaas/us60_pubcomb..pep:*	72	82.9	68	13	US-10-096-77-13	Sequence 39, Appl			
18: /cgn2_6_ptodata/1/pubpaas/us60_pubcomb..pep:*	72	82.9	68	14	US-10-044-992-40	Sequence 40, Appl			

RESULT 1
US-09-932-161-18
Sequence 18, Application US/09932161
Patent No. US20020037533A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
ORGANISATION: Lin, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932.161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FasSEQ for Windows Version 4.0
SEQ ID NO: 18
LENGTH: 20
TYPE: PRT
ORGANISM: Homo Sapien
US-09-932-161-18

RESULT 2
US-10-096-77-18
Sequence 18, Application US/10096777
Publication No. US20030171270A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
ORGANISATION: Lin, Steven
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932.161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FasSEQ for Windows Version 4.0
SEQ ID NO: 18
LENGTH: 20
TYPE: PRT
ORGANISM: Homo Sapien
US-09-932-161-18

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
					Sequence 18, Appl	Sequence 19, Appl
1	72	87.8	20	9	US-09-932-161-18	Sequence 15, Appl
2	72	87.8	20	14	US-10-096-77-18	Sequence 15, Appl
3	72	87.8	31	9	US-09-932-161-15	Sequence 15, Appl
4	72	87.8	31	14	US-10-096-77-15	Sequence 15, Appl
5	72	87.8	87	13	US-10-044-592-92	Sequence 92, Appl
6	68	82.9	19	13	US-10-044-592-27	Sequence 27, Appl
7	68	82.9	20	9	US-09-932-161-16	Sequence 16, Appl
8	68	82.9	20	13	US-10-044-592-42	Sequence 42, Appl
9	68	82.9	20	14	US-10-044-592-16	Sequence 16, Appl
10	68	82.9	21	13	US-10-044-592-16	Sequence 16, Appl
11	68	82.9	22	13	US-10-044-592-44	Sequence 44, Appl
12	68	82.9	31	9	US-09-932-161-13	Sequence 13, Appl
13	68	82.9	31	13	US-10-044-592-39	Sequence 39, Appl
14	68	82.9	31	14	US-10-044-592-13	Sequence 13, Appl
15	68	82.9	32	13	US-10-044-592-40	Sequence 40, Appl

; TITLE OF INVENTION: Therapeutic Compositions and Methods
 ; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
 ; FILE REFERENCE: P-UC 3534
 ; CURRENT APPLICATION NUMBER: US/10/096,777
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: US/09/560,915
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-096-777-18
 ;
 ; RESULT 5
 ; US-10-096-777-18
 ; Query Match 87.8%; Score 72; DB 14; Length 20;
 ; Best Local Similarity 100.0%; Pred. No. 6.2e-05;
 ; Matches 13; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
 ;
 ; Qy 2 AWYASRGIRPVGR 14
 ; Db 18 AWYASRGIRPVGR 30
 ;
 ; RESULT 5
 ; US-10-096-592-92
 ; Sequence 92, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fukushima, Shoji
 ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; FILE REFERENCE: 246JUS2P
 ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; CURRENT FILING DATE: 2002-01-10
 ; PRIORITY NUMBER: US 09/103639
 ; PRIOR FILING DATE: 1999-25-10
 ; PRIOR APPLICATION NUMBER: PCT/JP98/01923
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: JP 9-109974
 ; PRIOR FILING DATE: 1997-04-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE:
 ; SEQ ID NO 92
 ; LENGTH: 87
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-096-592-92
 ;
 ; Query Match 87.8%; Score 72; DB 13; Length 87;
 ; Best Local Similarity 100.0%; Pred. No. 0.00024;
 ; Matches 13; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
 ;
 ; Qy 2 AWYASRGIRPVGR 14
 ; Db 40 AWYASRGIRPVGR 52
 ;
 ; RESULT 6
 ; US-10-096-592-27
 ; Sequence 27, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fukushima, Shoji
 ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; FILE REFERENCE: 246JUS2P
 ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; CURRENT FILING DATE: 2002-01-10
 ; PRIORITY NUMBER: US 09/103639
 ; PRIOR FILING DATE: 1999-25-10
 ; PRIOR APPLICATION NUMBER: PCT/JP98/01923
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: JP 9-109974
 ; PRIOR FILING DATE: 1997-04-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE:
 ; SEQ ID NO 27
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Bovine
 ; US-10-096-592-27
 ;
 ; Query Match 82.9%; Score 68; DB 13; Length 19;
 ;
 ; RESULT 4
 ; US-10-096-777-15
 ; Sequence 15, Application US/10096777
 ; Publication No. US20030171270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Civelli, Olivier
 ; APPLICANT: Lin, Steven
 ; TITLE OF INVENTION: Therapeutic Compositions and Methods
 ; FILE REFERENCE: P-UC 3534
 ; CURRENT APPLICATION NUMBER: US/10/096,777
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: US/09/560,915
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 31
 ;
 ; Query Match 87.8%; Score 72; DB 9; Length 31;
 ; Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 ; Matches 13; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
 ;
 ; Qy 2 AWYASRGIRPVGR 14
 ; Db 18 AWYASRGIRPVGR 30
 ;
 ; RESULT 4
 ; US-10-096-777-15
 ; Sequence 15, Application US/10096777
 ; Publication No. US20030171270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Civelli, Olivier
 ; APPLICANT: Lin, Steven
 ; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
 ; FILE REFERENCE: P-UC 3534
 ; CURRENT APPLICATION NUMBER: US/10/096,777
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: US/09/560,915
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 31
 ;
 ; Query Match 82.9%; Score 68; DB 13; Length 19;

FILE REFERENCE: 2463US2P
 CURRENT APPLICATION NUMBER: US/10/044,592
 CURRENT FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US/09/403639
 PRIOR FILING DATE: 1999-05-10
 PRIOR APPLICATION NUMBER: PCT/JP98/01923
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: JP 9-109974
 PRIOR FILING DATE: 1997-04-28
 NUMBER OF SEQ ID NOS: 96
 SEQ ID NO 44
 LENGTH: 22
 TYPE: PRT
 ORGANISM: Bovine
 SOFTWARE: US-10-044-592-44

Query Match 82.9%; Score 68; DB 13; Length 22;
 Best Local Similarity 92.3%; Pred. No. 0.0003; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 14
 US-10-044-592-39
 Sequence 13, Application US/10096777
 Publication No. US2003010171270A1
 GENERAL INFORMATION:
 APPLICANT: Civelli, Olivier
 ATTORNEY OR AGENT: Lin, Steven
 TITLE OF INVENTION: Therapeutic Compositions and Methods
 Relating To Prolacatin Releasing Peptide (PrRP)
 FILE REFERENCE: P-UC 3534
 CURRENT APPLICATION NUMBER: US/10/096,777
 CURRENT FILING DATE: 2002-03-12
 PRIOR APPLICATION NUMBER: US/09/560,915
 PRIOR FILING DATE: 2000-04-28
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 13
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Bos taurus
 US-10-044-592-13

Query Match 82.9%; Score 68; DB 14; Length 31;
 Best Local Similarity 92.3%; Pred. No. 0.00042; Mismatches 1; Indels 0; Gaps 0;

Query Match 82.9%; Score 68; DB 14; Length 31;
 Best Local Similarity 92.3%; Pred. No. 0.00042; Mismatches 1; Indels 0; Gaps 0;

Query Match 82.9%; Score 68; DB 14; Length 31;
 Best Local Similarity 92.3%; Pred. No. 0.00042; Mismatches 1; Indels 0; Gaps 0;

Query Match 82.9%; Score 68; DB 9; Length 31;
 Best Local Similarity 92.3%; Pred. No. 0.00042; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 15
 US-10-044-592-40
 Sequence 40, Application US/10044592
 Publication No. US20020143152A1
 GENERAL INFORMATION:
 APPLICANT: Fukusumi, Shoji
 ATTORNEY OR AGENT: Fukusumi, Shoji
 TITLE OF INVENTION: Polypeptides, their Production and Use
 FILE REFERENCE: 2463US2P
 CURRENT APPLICATION NUMBER: US/10/044,592
 CURRENT FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US/09/403639
 PRIOR FILING DATE: 1999-05-10
 PRIOR APPLICATION NUMBER: PCT/JP98/01923
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: JP 9-109974
 PRIOR FILING DATE: 1997-04-28
 NUMBER OF SEQ ID NOS: 96
 SOFTWARE:
 SEQ ID NO 40
 LENGTH: 32
 TYPE: PRT
 ORGANISM: Bovine
 US-10-044-592-40

RESULT 13
 US-10-044-592-39
 Sequence 39, Application US/10044592
 Publication No. US20020143152A1
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 ATTORNEY OR AGENT: Fukusumi, Shoji
 TITLE OF INVENTION: Polypeptides, their Production and Use
 FILE REFERENCE: 2463US2P
 CURRENT APPLICATION NUMBER: US/10/044,592
 CURRENT FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US/09/403639
 PRIOR FILING DATE: 1999-05-10
 PRIOR APPLICATION NUMBER: PCT/JP98/01923
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: JP 9-109974
 PRIOR FILING DATE: 1997-04-28
 NUMBER OF SEQ ID NOS: 96
 SOFTWARE:
 SEQ ID NO 40
 LENGTH: 32
 TYPE: PRT
 ORGANISM: Bovine
 US-10-044-592-40

Query Match 82.9%; Score 68; DB 13; Length 32;
 Best Local Similarity 92.3%; Pred. No. 0.00043;
 Matches 12; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 2 ANYASGRIRPVGR 14
 Db 18 AWYAGRGIRPVGR 30

RESULT 16
 US-10-044-592-41
 ; Sequence 41, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiruma, Shuji
 ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; FILE REFERENCE: 246-US2P
 ; CURRENT FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 09/403639
 ; PRIOR FILING DATE: 1999-04-28
 ; PRIORITY NUMBER: PCT/JP98/01923
 ; PRIORITY NUMBER: US 09/403639
 ; PRIORITY NUMBER: JP 9-109974
 ; PRIORITY NUMBER: JP 9-109974
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE:
 ; SEQ ID NO: 41
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Bovine
 ; NUMBER OF SEQ ID NOS: 96

Query Match 82.9%; Score 68; DB 13; Length 32;
 Best Local Similarity 92.3%; Pred. No. 0.00044;
 Matches 12; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 2 ANYASGRIRPVGR 14
 Db 18 AWYAGRGIRPVGR 30

RESULT 17
 US-10-044-592-28
 ; Sequence 28, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiruma, Shuji
 ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; FILE REFERENCE: 246-US2P
 ; CURRENT FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 09/403639
 ; PRIORITY NUMBER: PCT/JP98/01923
 ; PRIORITY NUMBER: US 09/403639
 ; PRIORITY NUMBER: JP 9-109974
 ; PRIORITY NUMBER: JP 9-109974
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE:
 ; SEQ ID NO: 28
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: Marine

Query Match 82.9%; Score 68; DB 13; Length 32;
 Best Local Similarity 92.3%; Pred. No. 0.00012;
 Matches 12; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 2 ANYASGRIRPVGR 14
 Db 40 AWYAGRGIRPVGR 52

Query Match 82.9%; Score 68; DB 13; Length 32;
 Best Local Similarity 92.3%; Pred. No. 0.00043;
 Matches 12; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 2 ANYASGRIRPVGR 14
 Db 40 AWYAGRGIRPVGR 52

RESULT 18
 US-10-044-592-38
 ; Sequence 38, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fukusumi, Shoji
 ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; FILE REFERENCE: 246-US2P
 ; CURRENT FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 09/403639
 ; PRIORITY NUMBER: PCT/JP98/01923
 ; PRIORITY NUMBER: PCT/JP98/01923
 ; PRIORITY NUMBER: JP 9-109974
 ; PRIORITY NUMBER: JP 9-109974
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE:
 ; SEQ ID NO: 38
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: Bovine
 ; NUMBER OF SEQ ID NOS: 96

Query Match 82.9%; Score 68; DB 13; Length 32;
 Best Local Similarity 92.3%; Pred. No. 0.00012;
 Matches 12; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 2 ANYASGRIRPVGR 14
 Db 40 AWYAGRGIRPVGR 52

Query Match 82.9%; Score 68; DB 13; Length 32;
 Best Local Similarity 92.3%; Pred. No. 0.00012;
 Matches 12; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 2 ANYASGRIRPVGR 14
 Db 40 AWYAGRGIRPVGR 52

RESULT 20
 US-10-044-592-84
 ; Sequence 84, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; ; APPLICANT: Hinuma, Shuji
 ; ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; ; FILE REFERENCE: 2463US2P
 ; ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; ; CURRENT FILING DATE: 2002-01-10
 ; ; PRIOR APPLICATION NUMBER: US 09/403639
 ; ; CURRENT FILING DATE: 1999-05-10
 ; ; PRIOR APPLICATION NUMBER: PCT/JP98/01923
 ; ; CURRENT FILING DATE: 2002-01-10
 ; ; PRIOR APPLICATION NUMBER: US 09/403639
 ; ; NUMBER OF SEQ ID NOS: 96
 ; ; SEQ ID NO: 88
 ; ; LENGTH: 98
 ; ; TYPE: PRT
 ; ; ORGANISM: Bovine
 ; ; SOFTWARE:
 ; ; US-10-044-592-84

Query Match 82.9%; Score 68; DB 13; Length 98;
 Best Local Similarity 92.3%; Pred. No. 0.0012;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 40 AWYASRGIRPVGR 52

RESULT 23
 US-09-932-161-17
 ; Sequence 17, Application US/09932161
 ; Patent No. US20030037533A1
 ; GENERAL INFORMATION:
 ; ; APPLICANT: Civelli, Olivier
 ; ; ; APPLICANT: Lin, Steven
 ; ; ; TITLE OF INVENTION: Promoting and Therapeutic Methods For
 ; ; ; FILE REFERENCE: P-UC 4679
 ; ; ; CURRENT APPLICATION NUMBER: US/09/932,161
 ; ; ; CURRENT FILING DATE: 2001-08-17
 ; ; ; PRIOR APPLICATION NUMBER: US 09/560,915
 ; ; ; NUMBER OF SEQ ID NOS: 24
 ; ; ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; ; ; SEQ ID NO: 17
 ; ; ; LENGTH: 20
 ; ; ; TYPE: PRT
 ; ; ; ORGANISM: Rattus
 ; ; ; US-09-932-161-17

Query Match 82.9%; Score 68; DB 13; Length 98;
 Best Local Similarity 92.3%; Pred. No. 0.0012;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 40 AWYASRGIRPVGR 52

RESULT 24
 US-10-044-592-86
 ; Sequence 86, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; ; APPLICANT: Hinuma, Shuji
 ; ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; ; FILE REFERENCE: 2463US2P
 ; ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; ; CURRENT FILING DATE: 2002-01-10
 ; ; PRIOR APPLICATION NUMBER: US 09/403639
 ; ; CURRENT FILING DATE: 1999-05-10
 ; ; PRIOR APPLICATION NUMBER: PCT/JP98/01923
 ; ; CURRENT FILING DATE: 1999-04-28
 ; ; PRIOR APPLICATION NUMBER: JP 9-109974
 ; ; NUMBER OF SEQ ID NOS: 96
 ; ; SEQ ID NO: 86
 ; ; LENGTH: 98
 ; ; TYPE: PRT
 ; ; ORGANISM: Bovine
 ; ; SOFTWARE:
 ; ; US-10-044-592-86

Query Match 82.9%; Score 68; DB 13; Length 98;
 Best Local Similarity 92.3%; Pred. No. 0.0012;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 40 AWYASRGIRPVGR 52

RESULT 22
 US-10-044-592-88
 ; Sequence 88, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:

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; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; SOFTWARE: SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: antigen
US-10-044-592-6

; RESULT 27
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Rattus
; FEATURE: NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: antigen
US-10-044-592-6

; Query Match
; Best Local Similarity 78.0%;
; Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Score 64; DB 9; Length 31;
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Rattus
; FEATURE: NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: antigen
US-10-044-592-4

; Query Match
; Best Local Similarity 84.6%;
; Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Score 64; DB 9; Length 31;
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Rattus
; FEATURE: NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: antigen
US-10-044-592-4

; Sequence 4, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hiruma, Shuji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044-592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 4
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Murine
US-10-044-592-4

; Query Match
; Best Local Similarity 84.6%;
; Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Score 64; DB 13; Length 31;
; SEQ ID NO 4
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Murine
US-10-044-592-4

; Sequence 5, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hiruma, Shuji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044-592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 5
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: antigen
US-10-044-592-5

; Query Match
; Best Local Similarity 84.6%;
; Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Score 64; DB 14; Length 20;
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Rattus
; FEATURE: NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: antigen
US-10-044-592-5

; RESULT 28
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Rattus
; FEATURE: NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: antigen
US-10-044-592-6

; Sequence 14, Application US/09932161
; Patent No. US2002037533A1
; GENERAL INFORMATION:
; APPLICANT: Civelli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Promoting Wakefulness and Sleep
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: NAME/KEY: PEPTIDE
; LOCATION: (1)..(14)
; OTHER INFORMATION: antigen
US-10-044-592-6

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LOCATION: (1). (31)
 OTHER INFORMATION: antigen
 US-10-044-592-5

Query Match 78.0%; Score 64; DB 13; Length 31;
 Best Local Similarity 84.6%; Pred. No. 0.0019; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 2;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYTGRGIRPVGR 30

RESULT 31
 US-10-096-777-14
 ; Sequence 14, Application US/10096777
 ; Publication No. US20010171270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Civelli, Olivier
 ; INVENTION: Therapeutic Compositions and Methods
 ; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRP)
 ; FILE REFERENCE: P-UC 3534
 ; CURRENT APPLICATION NUMBER: US/10/096,777
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: US/09/560,915
 ; PRIOR FILING DATE: 2000-04-28
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 14
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Rattus
 US-10-096-777-14

Query Match 78.0%; Score 64; DB 14; Length 31;
 Best Local Similarity 84.6%; Pred. No. 0.0019; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 2;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYTGRGIRPVGR 30

RESULT 32
 US-10-044-592-96
 ; Sequence 96, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinuma, Shoji
 ; INVENTION: Polypeptides, their Production and Use
 ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; FILE REFERENCE: 2463US2P
 ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; CURRENT FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 09/403639
 ; PRIOR FILING DATE: 1999-05-10
 ; PRIOR APPLICATION NUMBER: PCT/JP98/01923
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: JP 9-109974
 ; PRIOR FILING DATE: 1997-04-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SEQ ID NO: 96
 ; LENGTH: 86
 ; TYPE: PRT
 ; ORGANISM: mammalian
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1224)..(1243)
 ; OTHER INFORMATION: Bracket region depicted in FIG 39.

Query Match 78.0%; Score 64; DB 13; Length 70;
 Best Local Similarity 84.6%; Pred. No. 0.004; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 2;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYTGRGIRPVGR 30

RESULT 33
 US-10-044-592-90
 ; Sequence 90, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinuma, Shoji
 ; INVENTION: Polypeptides, their Production and Use
 ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; FILE REFERENCE: 2463US2P
 ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; CURRENT FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 09/403639
 ; PRIOR FILING DATE: 1999-05-10
 ; PRIOR APPLICATION NUMBER: PCT/JP98/01923
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: JP 9-109974
 ; PRIOR FILING DATE: 1997-04-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SEQ ID NO: 90
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Rat
 US-10-044-592-90

Query Match 78.0%; Score 64; DB 13; Length 86;
 Best Local Similarity 84.6%; Pred. No. 0.0048; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 2;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYTGRGIRPVGR 30

1 / APPLICANT: Pena, Carol
 1 / APPLICANT: Burgess, Catherine
 1 / APPLICANT: Liu, Xiaohong
 1 / APPLICANT: Spytek, Kimberly
 1 / APPLICANT: Gorman, Linda
 1 / APPLICANT: Spaderna, Steven
 1 / APPLICANT: Voss, Edward
 1 / APPLICANT: Malvankar, Uriel
 1 / APPLICANT: Anderson, David
 1 / APPLICANT: Miller, Charles
 1 / APPLICANT: Taudier, Raymond J. Jr.
 1 / TITLE OF INVENTION: No. US20030208039A1 Antibodies that Bind to Antigenic Polypeptides
 1 / TITLE OF INVENTION: Encoding The Antigens, and Methods of Use.
 1 / FILE REFERENCE: 21402-290A (Cura 590AT)
 1 / CURRENT APPLICATION NUMBER: US10/993,463
 1 / CURRENT FILING DATE: 2002-06-24
 1 / PRIOR APPLICATION NUMBER: 60/283,675
 1 / PRIOR FILING DATE: 2001-04-14
 1 / PRIOR APPLICATION NUMBER: 60/338,092
 1 / PRIOR FILING DATE: 2001-12-03
 1 / PRIOR APPLICATION NUMBER: 60/274,281
 1 / PRIOR FILING DATE: 2001-03-08
 1 / PRIOR APPLICATION NUMBER: 60/274,101
 1 / PRIOR FILING DATE: 2001-03-08
 1 / PRIOR APPLICATION NUMBER: 60/225,681
 1 / PRIOR FILING DATE: 2001-09-27
 1 / PRIOR APPLICATION NUMBER: 60/304,354
 1 / PRIOR FILING DATE: 2001-07-10
 1 / PRIOR APPLICATION NUMBER: 60/279,995
 1 / PRIOR FILING DATE: 2001-03-30
 1 / PRIOR APPLICATION NUMBER: 60/294,899
 1 / PRIOR FILING DATE: 2001-05-31
 1 / PRIOR APPLICATION NUMBER: 60/287,424
 1 / PRIOR FILING DATE: 2001-04-30
 1 / PRIOR FILING DATE: 2001-06-18
 1 / PRIOR APPLICATION NUMBER: 60/309,198
 1 / PRIOR FILING DATE: 2001-07-31
 1 / PRIOR APPLICATION NUMBER: 60/281,194
 1 / PRIOR FILING DATE: 2001-04-04
 1 / PRIOR APPLICATION NUMBER: 60/274,194
 1 / PRIOR FILING DATE: 2001-03-08
 1 / PRIOR APPLICATION NUMBER: 60/274,849
 1 / PRIOR FILING DATE: 2001-03-09
 1 / PRIOR APPLICATION NUMBER: 60/330,380
 1 / PRIOR FILING DATE: 2001-10-18
 1 / PRIOR APPLICATION NUMBER: 60/275,235
 1 / PRIOR FILING DATE: 2001-03-12
 1 / PRIOR FILING DATE: 2001-05-03
 1 / PRIOR APPLICATION NUMBER: 60/275,578
 1 / PRIOR FILING DATE: 2001-03-13
 1 / NUMBER OF SEQ ID NOS: 370
 1 / SOFTWARE: PatentIn Ver. 2.1
 1 / SEQ ID NO: 188
 1 / LENGTH: 647
 1 / TYPE: PRT
 1 / ORGANISM: Homo sapiens
 US-10-093-463-188
 1 / APPLICANT: Chen, Xianfeng
 1 / APPLICANT: Cao, Yongwei
 1 / APPLICANT: Hinkle, Gregory J.
 1 / APPLICANT: Slater, Steven C.
 1 / APPLICANT: Goldman, Barry S.
 1 / APPLICANT: Chen, Xianfeng
 1 / TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 1 / FILE REFERENCE: 38-10 (52052) B
 1 / CURRENT APPLICATION NUMBER: US10/369,493
 1 / PRIOR FILING DATE: 2002-02-21
 1 / NUMBER OF SEQ ID NOS: 47374
 1 / SEQ ID NO: 12939
 1 / LENGTH: 411
 1 / TYPE: PRT
 1 / ORGANISM: Aspergillus nidulans
 1 / FEATURE:
 1 / NAME/KEY: unsure
 1 / LOCATION: (1) .. (411)
 1 / OTHER INFORMATION: unsure at all Xaa locations
 US-10-369-493-12939
 Qy 2 AWYASGIRPVGR 14
 Db 281 AWAESHLGLPIAR 293
 RESULT 38
 US-10-369-493-8457
 1 / Sequence 8457, Application US/10369493
 1 / GENERAL INFORMATION:
 1 / Publication No. US200302333675A1
 1 / APPLICANT: Cao, Yongwei
 1 / APPLICANT: Hinkle, Gregory J.
 1 / APPLICANT: Slater, Steven C.
 1 / APPLICANT: Goldman, Barry S.
 1 / APPLICANT: Chen, Xianfeng
 1 / TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 1 / FILE REFERENCE: 38-10 (52052) B
 1 / CURRENT APPLICATION NUMBER: US10/369,493
 1 / PRIOR FILING DATE: 2002-02-21
 1 / NUMBER OF SEQ ID NOS: 47374
 1 / SEQ ID NO: 8457
 1 / LENGTH: 555
 1 / TYPE: PRT
 1 / ORGANISM: Ralstonia metallidurans
 US-10-369-493-8457
 Qy 2 AWYASGIRPVGR 14
 Db 59 AWLQSRGLREGAR 71
 RESULT 39
 US-10-156 761-10748
 1 / Sequence 10748, Application US/10156761
 1 / GENERAL INFORMATION:
 1 / Publication No. US20030119018A1
 1 / APPLICANT: OMURA, SATOSHI

RESULT 37
 US-10-369-493-12939
 1 / Sequence 12939, Application US/10369493

APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 10748
 LENGTH: 402
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-10748

Query Match 52.4%; Score 43; DB 14; Length 402;
 Best Local Similarity 47.4%; Pred. No. 53; Matches 1; Indels 8; Gaps 1;
 Matches 9; Conservative 1; Mismatches 1;
 Qy 3 WYASRG-----IRPG 13
 Db 91 WYAPRGQSLRRAEIRPG 109

RESULT 40
 US-10-156-761-14927
 Sequence 14927, Application US/10156761
 Publication No. US0030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 14927
 LENGTH: 592
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-14927

Query Match 52.4%; Score 43; DB 14; Length 592;
 Best Local Similarity 72.7%; Pred. No. 76; Matches 2; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 2;
 Qy 2 AWYASRGIRPV 12
 Db 103 AWMAARGRPV 113

Search completed: February 25, 2004, 06:49:23
 Job time : 35 secs



Query Match 53.7%; Score 44; DB 2; Length 302;
 Best Local Similarity 70.0%; Pred. No. 8.6;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 A;Gene: AGR_C_2196
 A;Map position: circular chromosome

Query Match 51.2%; Score 42; DB 2; Length 105;
 Best Local Similarity 67.7%; Pred. No. 6.8;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 A;Gene: AGR_C_2196
 A;Map position: circular chromosome

Qy 2 AWYASRGIRP 11
 Db 126 AWYASRDLCQ 135

RESULT 3

S6 046
 ARPI protein - yeast (Saccharomyces cerevisiae)
 N; Alternate names: protein D1478; protein YDL17C
 C; Species: Saccharomyces cerevisiae
 C; Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
 R; Accession: S61046; S31139; S67719
 R; Pohl, T.M.
 submitted to the EMBL Data Library, November 1995
 A; Reference number: S61010
 A; Accession: S61046
 A; Molecule type: DNA
 A; Cross-references: EMBL:Z67750; PIDN:CAA91579.1; PID:gi061272
 R; Rehner, E.P.; Rao, E.; Brandel, M.
 M01. Gen. Genet. 237, 351-358, 1993
 A; Title: Molecular structure and genetic regulation of SPA, a gene responsible for resistance to the EMBL Data Library, August 1992
 A; Reference number: S31138; MUID:93247548; PMID:8433449
 A; Status: nucleic acid sequence not shown; translation not shown
 R; Pohl, T.M.
 submitted to the Protein Sequence Database, July 1996
 A; Reference number: S67708
 A; Accession: S67719
 A; Molecule type: DNA
 A; Cross-references: EMBL:Z74215; PIDN:CAA98741.1; PID:e253076; PID:gi143126
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R; Pohl, T.M.
 A; Experimental source: strain S288C
 C; Genetics:
 A; Gene: SGD:MRP1; ARP1
 A; Cross-references: MIPS:YDL167C; SGD:S0002326
 A; Map position: 4L

RESULT 4

A97505
 hypothetical protein AGR_C_2196 [Imported] - Agrobacterium tumefaciens (strain C58, Cereus sp.)
 C; Species: Agrobacterium tumefaciens
 C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quroollc, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Marzelz, B.; Science 294, 2323-2328, 2001
 A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A; Reference number: A97359; MUID:2160551; PMID:11743194
 A; Accession: A97505
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-105 <KUR>
 A; Cross-references: GB:IA000020; PIDN:BA878141.1; PID:gi17135595; GSPDB:GN00180

Qy 2 AWYASRGIRP 13
 Db 244 SWFTQGVFVG 255

RESULT 5

AE2723
 hypothetical protein Atul191 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C; Species: Agrobacterium tumefaciens
 C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C; Accession: AE2723
 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Erger, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyaviv, T.; Levy, R.; Li, M.; McClellan, R.; Kartp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.; E.W.
 A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A; Reference number: AB2577; MUID:21608550; PMID:11743193
 A; Accession: AE2723
 A; Molecule type: DNA
 A; Residues: 1-105 <KUR>
 A; Cross-references: GB:AB000688; PIDN:AA42203.1; PID:gi17739595; GSPDB:GN00186
 A; Status: preliminary
 A; Genetics:
 A; Gene: Atul191
 A; Map position: circular chromosome

Query Match 51.2%; Score 42; DB 2; Length 105;
 Best Local Similarity 67.7%; Pred. No. 6.8;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 A;Gene: Atul191
 A;Map position: circular chromosome

Qy 2 AWYASRGIR 10
 Db 54 AWYASRGVQ 62

RESULT 6

AI2484
 hypothetical protein alr7057 [Imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a1
 C; Species: Nostoc sp. PCC 7120
 C; Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C; Accession: AI2484
 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Iriuchishi, R.; Nakazaki, N.; Shinozaki, K.; Arai, K.; Takemoto, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120
 A; Reference number: AB1607; MUID:21593285; PMID:11759840
 A; Accession: AI2484
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-113 <KUR>
 A; Cross-references: GB:IA000020; PIDN:BA878141.1; PID:gi17135595; GSPDB:GN00180
 A; Genetics:
 A; Gene: alr7057
 A; Genome: plasmid

Query Match 51.2%; Score 42; DB 2; Length 113;
 Best Local Similarity 70.0%; Pred. No. 7.3;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 A;Gene: alr7057
 A;Map position: circular chromosome

Qy 2 AWYASRGIRP 11

Db 64 ANYAKAGIEP 73

Db 237 CAEBOLARPSSG 249

RESULT 7

BB424 protein-export membrane protein XF0304 [imported] - *Xylella fastidiosa* (strain 9a5c)C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #text_change 20-Aug-2000

C;Accession: BB2824

C;Anonymous: The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen-

C;Name: 406, 151-157, 2000

C;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

C;Reference number: A82515; MUID:10910347

C;Note: For complete list of authors see reference number A59328 below

C;Accession: BB3824

C;Status: preliminary

C;Molecule type: DNA

C;Residues: 1-132 <SIM>

C;Cross-references: GB:AE003883; GB:AE003849; PIDN:AAF83115; GSPDB:GN001

C;Experimental source: strain 9a5c

C;Accession: BB2824

C;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

C;Reference number: A82515; MUID:20365717; PMID:10910347

C;Note: For complete list of authors see reference number A59328 below

C;Accession: BB3824

C;Status: preliminary

C;Molecule type: DNA

C;Residues: 1-132 <SIM>

C;Cross-references: GB:AE003883; GB:AE003849; PIDN:AAF83115; GSPDB:GN001

C;Experimental source: strain 9a5c

C;Accession: BB2824

C;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

C;Reference number: A82515; MUID:10910347

C;Note: For complete list of authors see reference number A59328 below

C;Accession: BB3824

C;Status: preliminary

C;Molecule type: DNA

C;Residues: 1-132 <SIM>

C;Cross-references: GB:AE003883; GB:AE003849; PIDN:AAF83115; GSPDB:GN001

C;Experimental source: strain 9a5c

C;Accession: BB2824

C;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

C;Reference number: A82515; MUID:10910347

C;Note: For complete list of authors see reference number A59328 below

C;Accession: BB3824

C;Status: preliminary

C;Molecule type: DNA

C;Residues: 1-132 <SIM>

C;Cross-references: GB:AE003883; GB:AE003849; PIDN:AAF83115; GSPDB:GN001

C;Experimental source: strain 9a5c

C;Accession: BB2824

C;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

C;Reference number: A82515; MUID:10910347

C;Note: For complete list of authors see reference number A59328 below

C;Accession: BB3824

C;Status: preliminary

C;Molecule type: DNA

C;Residues: 1-132 <SIM>

C;Cross-references: GB:AE003883; GB:AE003849; PIDN:AAF83115; GSPDB:GN001

C;Experimental source: strain 9a5c

C;Accession: BB2824

C;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

C;Reference number: A82515; MUID:10910347

C;Note: For complete list of authors see reference number A59328 below

C;Accession: BB3824

C;Status: preliminary

C;Molecule type: DNA

C;Residues: 1-132 <SIM>

C;Cross-references: GB:AE003883; GB:AE003849; PIDN:AAF83115; GSPDB:GN001

C;Experimental source: strain 9a5c

C;Accession: BB2824

C;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

C;Reference number: A82515; MUID:10910347

RESULT 9

A95148 LicitD protein [imported] - *Streptococcus pneumoniae* (strain TIGR4)C;Species: *Streptococcus pneumoniae*

C;Date: 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: A95148

C;Title: Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held

C;Authors: Tetteh, K.; Nelson, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, M.; Umam, L.A.; Hickey, B.K.; Holt, T.E.

C;Reference number: A82515; MUID:10910347

C;Note: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

C;Accession: A95148

C;Status: preliminary

C;Molecule type: DNA

C;Residues: 1-266 <KUR>

C;Cross-references: GB:AE005672; PIDN:AAK75378.1; PMID:914972757; GSPDB:GN00164; TIGR:SP4

C;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP1274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75378.1; PMID:914972757; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

A;Genetics:

A;Gene: SP1274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75378.1; PMID:914972757; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

A;Genetics:

A;Gene: SP1274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75378.1; PMID:914972757; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

A;Genetics:

A;Gene: SP1274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75378.1; PMID:914972757; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

A;Genetics:

A;Gene: SP1274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75378.1; PMID:914972757; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

A;Genetics:

A;Gene: SP1274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75378.1; PMID:914972757; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

A;Genetics:

A;Gene: SP1274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75378.1; PMID:914972757; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

A;Genetics:

A;Gene: SP1274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75378.1; PMID:914972757; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

A;Genetics:

RESULT 10

G98015

LicitD Protein [imported] - *Streptococcus pneumoniae* (strain R6)C;Species: *Streptococcus pneumoniae*

C;Date: 22-Oct-2001 #text_change 22-Oct-2001

C;Accession: G98015

C;Title: Arnold, J.; Blaszcak, L.; Burgert, S.; DeHoff, B.S.; E

C;Authors: Hosking, J.A.; Albom Jr., W.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAuliffe, R.; Leiland, D.J.; Lee, R.; Winkler, M.E.

C;Reference number: 11

C;Note: Y. P.; Sun, P.M.; Winkler, M.E.

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

C;Reference number: 11

C;Note: J. Bacteriol. 183: 5709-5717, 2001

C;Title: Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.;

C;Authors: Martins, E.M.B.N.; Madero, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.

RESULT 11

E95936

hypothetical protein [imported] - *Sinorhizobium meliloti* (strain 1021) magaplasmid pSymBC;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: E95936

C;Title: Finan, T.M.; Neidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan

C;Authors: Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

C;Reference: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo

C;Cross-references: 1 CAVYASRGIRPVG 13

C;Contents:

C;Genetics:

C;Gene: PA1952

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-250 <STO>

A;Cross-references: GB:AE004622; GB:AE004091

A;Genome: plasmid

Query Match 49.4%; Score 40.5%; DB 2; Length 313;
Best Local Similarity 50.0%; Pred. No. 35; Mismatches 2; Indels 7; Gaps 1;

Matches 10; Conservative 1; Gaps 1;

Qy 2 AWAS-----RGIRPVGR 14
Db 285 AWASHTVRAAHRGVRAVGR 304

RESULT 16

E00837 Hypothetical protein Rv0295c - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Accession: E70837
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
C;Species: Saccharomyces cerevisiae
C;Accession: S54589; S14045; S48307; B55096
C;Status: preliminary; sequence revision 01-Sep-1995 #text_change 21-Jul-2000
R:Pearson, D.; Bowman, S.
A;Submitted to the EMBL Data Library, May 1995
A;Reference number: S54589
A;Accession: S54589
A;Molecule type: DNA
A;Residues: 1-580 <PEA>
A;Cross-references: EMBL:Z49704; PID:9825540; PMID:CAA89780..1; PID:9825548; MIPS:YMR282C
A;Experimental source: strain AB972
R:Finnean, P.M.; Payne, M.J.; Keramidaris, B.; Lukins, H.B.
R:Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 37-54, 1998
A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Residues: 1-267 <COL>
A;Reference number: A70500; PMID:98295987; PMID:9634230
A;Accession: E70837
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: GB:AL021930; GB:AL123456; PID:93261524; PMID:e125247
A;Experimental source: strain H37RV
C.Genetics:
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0295c

Query Match 48.8%; Score 40%; DB 2; Length 267;
Best Local Similarity 54.5%; Pred. No. 36; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 3;

Qy 2 ANYASRGIRPV 12
Db 197 AWFAEEGGIDPI 207

RESULT 17

B75254 acetate kinase - Deinococcus radiodurans (strain R1)

C.Species: Deinococcus radiodurans
C.Accession: B75254
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Species: Saccharomyces cerevisiae
C;Accession: S54589; S14045; S48307; B55096
C;Status: preliminary
R:White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Ma, S.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 157-157, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75254; PMID:20036896; PMID:10567266
A;Accession: B75254
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 <WHL>
A;Cross-references: GB:AB0002089; GB:AB000513; PID:96460427; PMID:AAF12139..1; PID:9646042
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2602
A;Map position: 1
C;Superfamily: acetate kinase

Query Match 48.0%; Score 40%; DB 2; Length 398;
Best Local Similarity 50.0%; Pred. No. 53; Mismatches 2; Indels 4; Gaps 0;

Matches 6; Conservative 2;

Qy 2 ANYASRGIRPVG 13
Db 161 AWTSQHGGVRRYRG 172

RESULT 18

S54589 AEP2 protein - Yeast (Saccharomyces cerevisiae)
C.Species: Arp13 protein; protein YMR801..08c; protein YMR282c
C;Accession: S54589; S14045; S48307; B55096
C;Status: preliminary
R:Pearson, D.; Bowman, S.
A;Submitted to the EMBL Data Library, May 1995
A;Reference number: S54589
A;Accession: S54589
A;Molecule type: DNA
A;Residues: 1-337,'W',339-480,'V',482-580 <FIN>
A;Cross-references: EMBL:MS5960; PID:171033; PID:9171034
R:Ackerman, S.H.; Gatti, D.L.; Gallefors, P.; Douglas, M.G.; Tzagoloff, A.
PEBS Lett. 278, 234-238, 1991
A;Title: Characterization of a yeast nuclear gene, AEP2, required for accumulation of mi
A;Reference number: S19045; PMID:92035073; PMID:1718609
A;Accession: S19045
A;Molecule type: DNA
A;Residues: 1-337,'W',339-480,'V',482-580 <FIN>
A;Cross-references: EMBL:MS5960; PID:171033; PID:9171034
R:Ackerman, S.H.; Gatti, D.L.; Gallefors, P.; Douglas, M.G.; Tzagoloff, A.
PEBS Lett. 278, 234-238, 1991
A;Title: Atp13, a nuclear gene of *Saccharomyces cerevisiae* essential for the expression
A;Reference number: S14053; PMID:9122292; PMID:1825065
A;Accession: S14053
A;Molecule type: DNA
A;Residues: 1-213,'N',215-362,'TIVP',367,'YSFQS'
A;Cross-references: EMBL:MS6215; PID:93394; PMID:95679710
R:Astrom, S.U.; Bytrom, A.S.
A;Description: Ril1, a tRNA backbone modifying enzyme that mediates initiator/elongator
A;Title: Ril1, a tRNA backbone-modifying enzyme that mediates initiator/elongator
A;Reference number: S48306
A;Accession: S48307
A;Molecule type: DNA
A;Residues: 1-108 <AST>
A;Cross-references: EMBL:X80995; PID:9556674; PMID:CAA56771..1; PID:9556676
R:Aastrom, S.U.; Bytrom, A.S.
Cell 79, 535-546, 1994
A;Title: Ril1, a tRNA backbone-modifying enzyme that mediates initiator and elongator tRNA
A;Accession: B55096
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: EMBL:X80995; PID:9556674; PMID:9556676
A;Residues: 1-11,'V',13-108 <ASW>
A;Cross-references: EMBL:X80995
A;Note: authors translated the codon TGG for residue 2 as Thr, and GAT for residue 80 as
C;Genetics:
A;Gene: SGD:APB2; ATP13
A;Cross-references: SGD:S0004895; MIPS:YMR282C
A;Map position: 13R
A;Genome: nuclear
C;Function:
A;Description: required for the expression of ATP synthase subunit 9
C;Superfamily: Saccharomyces cerevisiae AEP2 protein
C;Keywords: mitochondrion
Query Match 48.8%; Score 40%; DB 2; Length 580;
Best Local Similarity 66.7%; Pred. No. 76; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;

Qy 3 WYASRGIRP 11
Db 439 WYASRKLRP 447

RESULT 19

I64045 recombination protein rec2 - Haemophilus influenzae (strain Rd KW20)

H82925 hypothetical protein uul63 [Imported] - Ureaplasma urealyticum
 C;Species: Ureaplasma urealyticum
 C;Accession: H82925
 R;Glass, J.J.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H.
 Submitted to GenBank, February 2000
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor
 A;Reference number: A82870
 A;Accession: H82925
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-260 <GLA>
 A;Cross-references: GB:AE002116; GB:AF222894; NID:96899118; PIDN:AAF30569.1; GSPDB:GN001
 A;Experimental source: serovar 3; biovar 1
 C;Genetics:
 A;Gene: UU163
 A;Genetic code: SGCG
 Query Match
 Best Local Similarity 47.6%; Score 39; DB 2; Length 260;
 Matches 6; Conservative 54.5%; Pred. No. 52; Gaps 0;
 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 WYASRGRIPVG 13
 Db 176 WYASDGVGKIG 186

RESULT 27
 A87709 formamidopyrimidine-DNA glycosylase CC3707 [Imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Accession: A87709
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.R.; Heidelberg, J.F.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolon, J.; Ermolaeva, M.O.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; PMID:21173698; PMID:11259647
 A;Accession: A87709
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-315 <SP0>
 A;Cross-references: GB:AE005673; NID:913425473; PIDN:AAF25669.1; GSPDB:GN00148
 C;Genetics:
 A;Gene: CC3707
 C;Superfamily: formamidopyrimidine-DNA glycosidase

Query Match
 Best Local Similarity 47.6%; Score 39; DB 2; Length 315;
 Matches 6; Conservative 50.0%; Pred. No. 62; Gaps 0;
 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AWYASRGRIPVG 13
 Db 168 AWFAAMGEFPGL 179

RESULT 28
 H82852 hydroxybenzoate octaprenyltransferase Xp0068 [Imported] - Xylella fastidiosa (strain 9as)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
 R;Accession: H82852
 R;Anonymous The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: For a complete list of authors see reference number A59328 below
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-333 <SIM>

A;Cross-references: GB:AE003860; GB:AE003849; NID:99104830; PIDN:AAF82881.1; GSPDB:GN001
 A;Experimental source: strain 9as
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, J.E.A.; Carrasco, A.P.; Ferreira, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 Submitted to GenBank, June 2000
 A;Author: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Juncqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigr
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marques, M.V.; Martins, E
 A;Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Mirrach, E.C.; Miyaki, C.Y.
 P.G.; Nunes, L.R.; Oliveira, M.A.; Oliveira, R.C.; Palmieri, D.A.
 Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A;Author: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, M.; Tsunahiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XF0068
 C;Superfamily: 4-hydroxybenzoate octaprenyltransferase
 Query Match
 Best Local Similarity 47.6%; Score 39; DB 2; Length 333;
 Matches 7; Conservative 63.6%; Pred. No. 66; Gaps 0;
 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 WYASRGRIPVG 13
 Db 58 WLGRDGRIPVG 68

RESULT 27
 G7047 hypothetical protein Rv3169 - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Accession: G7047
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
 ; Connor, R.; Davies, R.; Devlin, K.; Feilwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A;Author: Squires, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:9825987; PMID:9634230
 A;Accession: G70947
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-374 <COL>
 A;Cross-references: GB:AL021646; GB:AL123456; PIDN:CAA16634.1; PID:e124876
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: Rv3169

Query Match
 Best Local Similarity 47.6%; Score 39; DB 2; Length 374;
 Matches 9; Conservative 60.0%; Pred. No. 73; Gaps 1;
 0; Mismatches 2; Indels 4; Gaps 1;

Qy 3 WYASR---GIRPYG 13
 Db 171 WLGRDGRIPVG 185

RESULT 28
 B38176 *Salmonella typhimurium*
 C;Species: *Salmonella typhimurium*
 C;Accession: B38176
 R;Nohmi, T.; Hakura, A.; Nakai, Y.; Watanabe, M.; Murayama, S.Y.; Sofuni, T.
 J.; Bacteriol. 173, 1051-1063, 1991
 A;Title: *Salmonella typhimurium* has two homologous but different umuDC operons: cloning
 A;Reference number: A38176; MUID:91123176; PMID:1991707
 A;Accession: B38176
 A;Status: Preliminary
 A;Molecule type: DNA

A;Residues: 1-424 <NOH>
 A;Cross-references: GB:D90202; NID:9217087; PIDN:BA014226.1; PMID:9217089
 A;Experimental source: strain LT2
 C;Genetics:
 A;Gene: samB
 C;Function:
 A;Description: restores JV mutability, involved in mutagenesis
 C;Keywords: umuc protein
 C;Superfamily: DNA repair, induced mutagenesis; SOS mutagenesis

Query Match 47.6%; Score 39; DB 2; Length 424;
 Best Local Similarity 66.7%; Pred. No. 83;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 WYARGIRGP 11
 Db 390 WFAGRGIAAP 398

RESULT 29
 AB034 UV protection protein [Imported] - *Salmonella enterica* subsp. *enterica* serovar *Typhi* (strain AB034)
 C;Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB1034
 R;Parchmill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Moulou, S.; O'Gara, P.
 Nature 413, 848-852, 2001
 A;Authors: Party, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; E91019
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar *Enterica* [Imported] - *Escherichia coli* (strain E91019)
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AB1034
 A;Molecule type: DNA
 A;Residues: 1-424 <PAR>
 A;Cross-references: GB:AL51382; PIDN:CAD06719.1; PMID:916505372; GSPDB:GN00176
 C;Genetics:
 A;Gene: samB
 C;Superfamily: umuc protein

Query Match 47.6%; Score 39; DB 2; Length 424;
 Best Local Similarity 66.7%; Pred. No. 83;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 WYARGIRGP 11
 Db 390 WFAGRGIAAP 398

RESULT 30 JN0EGT 91-glycerol-3-phosphate transloc protein - *Escherichia coli* (strain K-12)
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 01-Mar-2002
 C;Accession: S00868; F00994
 R;Eiglmeier, K.; Boos, W.; Cole, S.T.
 Mol Microbiol. 1, 251-258, 1987
 A;Title: Nucleotide sequence and transcriptional startpoint of the *glpT* gene of *Escherichia coli* 91-glycerol-3-phosphate transloc protein - *Escherichia coli* (strain K-12)
 A;Reference number: S00868; MUID:3323281; PMID:88201663;
 A;Molecule type: DNA
 A;Residues: 1-452 <EIG>
 A;Cross-references: EMBL:Y00536; NID:941586; PIDN:CAA68598.1; PID:941587
 A;Experimental source: strain K12
 R;Blattner, F.R.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca, A.;Title: Genome sequence of *enterohemorrhagic Escherichia coli* O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:1120551
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:97426617; PMID:97426603
 A;Status: preliminary

A;Accession: F64994
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-452 <BLAT>
 A;Cross-references: GB:AE000314; PIDN:91788570; PID:91788575;
 A;Experimental source: strain K-12, substrain MG1655
 C;Genetics:
 A;Gene: glpT
 A;Map position: 49 min
 C;Superfamily: hexose phosphate transport protein upbT
 C;Keyword: sugar phosphate transport system; transmembrane protein
 F;94-117/Domain: transmembrane #sttus predicted <TM1>
 F;120-138/Domain: transmembrane #status predicted <TM2>
 F;167-183/Domain: transmembrane #status predicted <TM3>
 F;186-208/Domain: transmembrane #status predicted <TM4>
 F;254-273/Domain: transmembrane #status predicted <TM5>
 F;322-341/Domain: transmembrane #status predicted <TM6>
 F;351-373/Domain: transmembrane #status predicted <TM7>
 F;382-406/Domain: transmembrane #status predicted <TM8>
 F;415-437/Domain: transmembrane #status predicted <TM9>

Query Match 47.6%; Score 39; DB 1; Length 452;
 Best Local Similarity 42.9%; Pred. No. 88;
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 CAWTASRGIRGPVGR 144
 Db 130 CGWFQGMGNPPCGR 143

RESULT 31
 sn-Glycerol-3-phosphate permease [Imported] - *Escherichia coli* (strain O157:H7, substrain E91019)
 C;Species: *Escherichia coli*
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C;Accession: E91019
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawara, N.; Yasunaga, T.; Kubara, S.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of *enterohemorrhagic Escherichia coli* O157:H7 and *Geno*
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: E91019
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-452 <HAY>
 A;Cross-references: GB:BA00007; PIDN:BA03548.1; PMID:91362595; GSPDB:GN00154
 C;Genetics:
 A;Gene: E9s3125
 C;Superfamily: hexose phosphate transport protein upbT
 C;Keyword: sugar phosphate transport system upbT
 F;94-117/Domain: transmembrane #sttus predicted <TM1>
 F;120-138/Domain: transmembrane #status predicted <TM2>
 F;167-183/Domain: transmembrane #status predicted <TM3>
 F;186-208/Domain: transmembrane #status predicted <TM4>
 F;254-273/Domain: transmembrane #status predicted <TM5>
 F;322-341/Domain: transmembrane #status predicted <TM6>
 F;351-373/Domain: transmembrane #status predicted <TM7>
 F;382-406/Domain: transmembrane #status predicted <TM8>
 F;415-437/Domain: transmembrane #status predicted <TM9>

Query Match 47.6%; Score 39; DB 2; Length 452;
 Best Local Similarity 42.9%; Pred. No. 88;
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 CAWTASRGIRGPVGR 144
 Db 130 CGWFQGMGNPPCGR 143

RESULT 32
 G85863 sn-Glycerol-3-phosphate permease [Imported] - *Escherichia coli* (strain O157:H7, substrain E91019)
 C;Species: *Escherichia coli*
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C;Accession: G85863
 R;Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca, A.;Title: Genome sequence of *enterohemorrhagic Escherichia coli* O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:1120551
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:97426617; PMID:97426603
 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-452 <STO>
 A;Cross-references: GB:AE005174; NID:912516580; PIDN:AGG57371.1; GSPDB:GN00145; UNGP:2334
 A;Experimental source: Strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: glpT
 C;Superfamily: hexose phosphate transport protein unpt

Query Match 47.6%; Score 39; DB 2; Length 452;
 Best Local Similarity 42.9%; Pred. No. 88;
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAYWASRGIRPVGR 14
 DB 130 CGFQGMWPPPCR 143

RESULT 33

T43558 sulfide dehydrogenase (coenzyme Q2) (EC 1.8.5.-) precursor, mitochondrial [validated] -
 C;Species: Schizosaccharomyces pombe
 C;Accession: T43558; T40163
 R;Vande Weghe, J.G.; Ow, D.W.
 J;Biol. Chem. 274, 13250-13257, 1999
 A;Title: A fission yeast gene for mitochondrial sulfide oxidation.
 A;Reference number: Z22577; MUII:99240711; PMID:10224084
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-459 <VAN>
 A;Cross-references: EMBL:AF042283; NID:95256827; PIDN:ADD41159.1; PID:95256828
 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Ielrae, V.; Galibert, F.
 Submitted to the EMBL Data Library, October 1998
 A;Reference number: Z21908
 A;Accession: T40163
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-459 <WOO>
 A;Cross-references: EMBL:AU03395; PIDN:CAA21882.1; GSPDB:GN00067; SPDB:SPBC2G5_06C
 A;Experimental source: strain 972h-; cosmid c2G5
 C;Genetics:
 A;Gene: hmt2; SPBC2G5_06C
 A;Map position: 2
 C;Function:
 A;Description: catalyzes the reduction of quinone (coenzyme Q2) by sulfide [validated]. M
 A;Note: Proposed to function as a sulfide quinone oxidoreductase
 C;Keywords: mitochondrial, oxidoreductase
 P;1-24/Domain: transit peptide (mitochondrion) #status Predicted <TNP>
 P;25-459/Product: sulfide dehydrogenase, mitochondrial #status Predicted <MAT>

Query Match 47.6%; Score 39; DB 2; Length 459;
 Best Local Similarity 66.7%; Pred. No. 89;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WYASRGIRPV 11
 DB 445 WYGSGLIP 453

RESULT 34

D84258 alcohol dehydrogenase [imported] - Halobacterium sp. NRC-1
 C;Species: Halobacterium sp. NRC-1
 C;Accession: D84258
 R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablek, T.; Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Babbard, H.; Lowe, T.M.; Li

A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: D84258
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-600 <STO>
 A;Cross-references: GB:AE004437; NID:910580574; PIDN:AGG19432.1; GSPDB:GN00138
 C;Genetics:
 A;Gene: adh3
 C;Superfamily: adh3

Query Match 47.6%; Score 39; DB 2; Length 600;
 Best Local Similarity 45.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 AWYASRGIRPV 12
 DB 552 AWHCIRGVVPI 562

RESULT 35

A35548 319K protein ndvB - Rhizobium meliloti
 C;Species: Rhizobium meliloti
 C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 08-Oct-1999
 C;Accession: A35548
 R;Ielpi, L.; Dylan, T.; Ditta, G.S.; Helinski, D.R.; Stanfield, S.W.
 J. Biol. Chem. 265, 2843-2851, 1990
 A;Title: The ndvB locus of Rhizobium meliloti encodes a 319-kDa protein involved in the
 A;Reference number: A35548; MUID:90153914; PMID:2154461
 A;Accession: A35548
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-2870 <IEL>
 A;Cross-references: GB:U05219; NID:9152270; PIDN:AAA26305.1; PID:9152271
 C;Keywords: transmembrane protein

Query Match 47.6%; Score 39; DB 2; Length 2870;
 Best Local Similarity 50.0%; Pred. No. 5.2e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 WYASRGIRPV 12
 DB 1126 WYRTTGLEPM 11356

RESULT 36

H72507 36K protein APE2038 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
 C;Accession: H72507
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Funahashi, T.; Tanaka, T.; Kawa, H.; Takamiya, M.; Masuda, S.; DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic thermophilic Crenarchaeon, Aeropyrum pernix K1
 A;Reference number: A72450; MUID:9931039; PMID:10382966
 A;Accession: H72507
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-121 <KAW>
 A;Experimental source: strain K1
 C;Superfamily: Aeropyrum pernix hypothetical protein APE2038
 A;Gene: APE2038
 C;Genetics:
 A;Accession: DDBJ:AP000063; NID:95105654; PIDN:BA81048.1; PID:di1044834; PID:95105654

Query Match 46.3%; Score 38; DB 2; Length 121;
 Best Local Similarity 50.0%; Pred. No. 37;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAYWASRGIRPVGR 14
 DB 43 CGYARSSIRTPAR 56

RESULT 37
 D87357 hypothetical protein C08711 [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C;Accession: D87357
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; Laub, M.T.; Debay, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolon, N.; J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11253647
 A;Accession: D87357
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-194 <STO>
 A;Cross-references: GB:AB005673; NID:913422132; PIDN:AAK22856.1; GSPDB:GN00148
 C;Genetics:
 A;Gene: CC08711

RESULT 40
 S68784
 cathepsin L - Paramecium tetraurelia (fragment)
 C;Species: Paramecium tetraurelia
 C;Date: 15-Feb-1997 #text_change 03-Nov-2000
 C;Accession: S68784
 R;Voeikel, H.; Kurz, U.; Linder, J.; Klumpp, S.; Gnau, V.; Jung, G.; Schultz, J.E.; Eur. J. Biochem. 238, 198-206, 1996
 A;Title: Cathepsin L is an intracellular and extracellular protease in Paramecium tetraurelia
 A;Reference number: S68783; MUID:86248439; PMID:8665938
 A;Accession: S68784
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-294 <STO>
 A;Cross-references: EMBL:X91756; NID:91403088; PID:220702; PID:91403089
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1995
 C;Genetics:
 A;Gene: H72646
 C;Accession: H72646
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrospacilicoccus sp. strain K1
 A;Accession: A72450; MUID:99310339; PMID:10382966
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-338 <KAW>
 A;Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BA979576.1; PID:d1043362; PID:9510
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE00606

RESULT 38
 H72646
 hypothetical protein APE00606 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C;Accession: H72646
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrospacilicoccus sp. strain K1
 A;Accession: A72450; MUID:99310339; PMID:10382966
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-338 <KAW>
 A;Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BA979576.1; PID:d1043362; PID:9510
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE00606

RESULT 39
 F95120
 hydrolase, probable [imported] - Streptococcus pneumoniae (strain TIGR4)
 C;Species: Streptococcus pneumoniae
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 02-Jun-2003
 C;Accession: F95120
 R;Fettelein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidorn, J.D.; Ummey, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel, T.; Ricket, E.K.; Holt, I.E.;
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A;Reference number: A95000; MUID:21357209; PMID:11463916
 A;Accession: F95120
 A;Status: preliminary

Search completed: February 25, 2004, 06:44:24
 Job time : 21 secs

Scoring table:	BLOSUM62	RESULT 1
Gapop:	10.0 , Gapext 0.5	PRRP_HUMAN STANDARD; PRT; 87 AA.
Searched:	141681 seqs, 52070155 residues	AC P81777; PRRP_HUMAN STANDARD; PRT; 87 AA.
Total number of hits satisfying chosen parameters:	141681	AC P81777; PRRP_HUMAN STANDARD; PRT; 87 AA.
Minimum DB seq length: 0		DT 30-MAY-2000 (Rel. 39, Created)
Maximum DB seq length: 2000000000		DT 30-MAY-2000 (Rel. 39, Last sequence update)
Post-processing: Minimum Match 0%		DT 28-FEB-2003 (Rel. 41, Last annotation update)
Post-processing: Maximum Match 100%		DB Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP20].
Database :	SwissProt_42:*	DE DE
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	DE DE
		GN Homo sapiens (Human).
		OS Homo sapiens (Human).
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		NCBI_TaxID=9606;
		RN [1]
		RP SEQUENCE FROM N.A.
		RC TISSUE=Brain;
		RX MEDLINE=98268781; PubMed=9607765;
		RA Hiruma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
		RA Kitada C., Maeda Y., Asano T., Matsunoto H., Sekiguchi M.,
		RA Kurokawa T., Nishimura O., Onda H., Fujino M.,
		RA RT "A prolactin-releasing peptide in the brain.";
		RL Nature 393:272-276(1998).
		RN [2]
		RP TISSUE SPECIFICITY.
		RX MEDLINE=99426552; PubMed=10498338;
		RA Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hiruma S.,
		RA Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
		RA PA Sumino Y., Fujino M.,
		RT "Tissue distribution of prolactin-releasing peptide (PrRP) and its receptor.";
		RL Regul. Pept. 83:1-10(1999).
		CC -!- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
		CC -!- TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.
		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. There is no way to remove this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
		CC EMBL; AB015419; BAA29027.1; -.
		DR MIM; 602663; -.
		DR GO; GO:0005180; F:peptide hormone; TAS.
		CC Hormone; Amidation; Signal.
		KW BY SIMILARITY.
		FT SIGNAL 1 22
		FT PROLTIN-RELEASING PEPTIDE PRRP31.
		FT PEPTIDE 23 53
		FT PROLTIN-RELEASING PEPTIDE PRRP20.
		FT PEPTIDE 34 53
		FT PROREP 58 53
		FT MOD_RES 53 53
		SEQUENCE 87 AA; 9639 MW; 229AA2F3F5OCF9B1B CRC64; 33

Qy	2 AWYASRGIRPGVR 14	Db	39 AWYTGGRGIRPGVR 51	Db	244 SWFTIQGVTPVG 255
RESULT 4					
NRP1_YEAST	STANDARD;	PRT;	719 AA.	RESULT 5	
ID_NRP1_YEAST				GLGB STRAW	STANDARD;
AC_P32770_1_Q12228;				ID_GLGB STRAW	PRT;
DT_AC_93247545 (Rel. 27, Created)				Q82JF0;	838 AA.
DT_01-OCT-1993 (Rel. 35, Last sequence update)				AC_10-OCT-2003 (Rel. 42, Created)	
DT_28-FEB-2003 (Rel. 41, Last annotation update)				DT_10-OCT-2003 (Rel. 42, Last annotation update)	
DE_Asparagine-rich Protein (ARP protein).				DE_1,4-alpha-D-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching enzyme) (BE) (1,4-alpha-D-Glucan:1,4-alpha-D-glucan 6-Glucosyl-transferase).	
GN_NRP1 OR ARP1 OR ARP OR YDL167C.				DE_GLGB OR SAV2805.	
OS_Saccharomyces cerevisiae (Baker's yeast).				OS_Strptomyces avermitillii.	
OC_Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomyces.				OC_Bacteria; Actinobacteria; Actinomycetales; Streptomyces.	
OC_NCB_TaxID=4932;				OC_Streptomyces; Streptomyctaceae; Streptomyces.	
RN_11]				OX_NCB_TaxID=31903;	
RP_SEQUENCE FROM N.A.				RN_RN	
RC_STRAIN=AH22;				RP_SEQUENCE FROM N.A.	
EX_MEDLINE=93247545; PubMed=8483449;				RC_STRAIN=NA-4610 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	
RA_Wehner E.P.; Rao E.; Brendel M.;				RC_MEDLINE=21477403; PubMed=11572948;	
RT_Molecular structure and genetic regulation of SFA, a gene				RA_Omura S.; Ikeda H.; Ishikawa J.; Hanamoto A.; Takahashi C.;	
RT_responsible for resistance to formaldehyde in <i>Saccharomyces</i>				RA_Sakimura M.; Takahashi Y.; Horikawa H.; Onoae T.,	
RT_cerevisiae, and characterization of its protein product.;"				RA_Kikuchi H.; Shiba T.; Sakai Y.; Hattori M.;	
RL_Nat. Genet. 23:7:351-358 (1993).				RT_Genomic sequence of an industrial microorganism Streptomyces avermitillii: deducing the ability of producing secondary metabolites.;	
RN_12]				RT_Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).	
RP_SEQUENCE FROM N.A.				RN_RN	
RC_STRAIN=ES288C;				RP_SEQUENCE FROM N.A.	
RA_Pohl T.M.;				RC_STRAIN=NA-4610 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	
RL_Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.				RC_MEDLINE=2260306; PubMed=12692552;	
CC_1-SIMILARITY: Contains 2 RANBP2-type zinc fingers.				RA_Ikeda H.; Ishikawa J.; Hanamoto A.; Shinose M.; Kikuchi H.; Shiba T.,	
CC_1-SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.				RA_Sakai Y.; Hattori M.; Omura S.;	
CC_This SWISS-PROT entry is copyright. It is produced through a collaboration				RT_RT	
CC_between the Swiss Institute of Bioinformatics and the EMBL outstation -				RT_Complete genome sequence and comparative analysis of the industrial	
CC_the European Bioinformatics Institute. There are no restrictions on its				RT_microorganism Streptomyces avermitillii.;"	
CC_use by non-profit institutions as long as its content is in no way				CC_RL_BioTechnol. 21:526-531 (2003).	
CC_modified and this statement is not removed. Usage by and for commercial				CC_1-FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic	
CC_entities requires a license agreement (See http://www.isb-sib.ch/announce/				CC_linkages in glycogen by scission of a 1,4-alpha-linked	
CC_or send an email to license@isb-sib.ch).				CC_oligosaccharide from growing alpha-1,4-glucan chains and the	
CC				CC_subsequent attachment of the oligosaccharide to the alpha-1,6	
CC				CC_position (By similarity).	
CC				CC_1-CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of	
CC				CC_glycogen.	
CC				CC_1-PATHWAY: Glycogen biosynthesis; third step.	
CC				CC_1-SUBUNIT: Monomer (By similarity).	
CC				CC_1-SIMILARITY: Belongs to family 13 of glycosyl hydrolases.	
DR_EMBL: Z68020; CA048159.1; -				CC	
DR_EMBL: Z67750; CA049157.1; -				CC	
DR_PIR: S61046; S61046.				CC	
DR_GermOnline: 140410; -.				CC	
DR_SGD; SGD0002326; NRP1.				CC	
DR_InterPro; IPR0001876; Znf_RanGDP.				CC	
DR_Pfam; PF00076; zrm; 1.				CC	
DR_Pfam; PF00641; zf-Ramp; 2.				CC	
DR_SMART; SM00360; RRM; 1.				CC	
DR_SMART; SM00547; znf_RBZ; 2.				CC	
DR_Posite; PS50102; RRM; 1.				CC	
DR_Posite; PS00030; RRM_RNP_1; FALSE_NEG.				CC	
DR_Posite; PS01358; ZFP_RANBP2; 2.				CC	
DR_Posite; PS50199; ZFP_RANBP2; 2.				CC	
KW_Nuclear Protein; Zinc-finger; RNA-binding; Repeat.				CC	
FT_DOMAIN 226				DR_HAMP; MF_00655; -; 1.	
FT_ZN_FING 355				DR_InterPro; IPR006589; Alpha_amyl_cat_sub.	
FT_ZN_FING 581				DR_InterPro; IPR00604; Alpha_amyl_cat.	
FT_DOMAIN 493				DR_InterPro; IPR006407; G19B.	
FT_CONFLICT 493				DR_InterPro; IPR004193; Glyco_hydro_13N.	
SEQ_SEQUENCE 719 AA;				DR_Pfam; PF0018; alpha_amylase; 1.	
Score Match 53.7%; Score 44; DB 1; Length 719;				DR_SMART; SM00642; Amy; 1.	
Best Local Similarity 50.0%; Prod. No. 5.6;				DR_TIGRFAMS; TIGR0155; branching_enzym; 1.	
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;				KW_Glycogen biosynthesis; Transferase; Glycosyltransferase;	
				KW_Complete proteome.	
				FT_ACT_SITE 408	BY SIMILARITY.
				FT_ACT_SITE 443	BY SIMILARITY.
				FT_ACT_SITE 448	BY SIMILARITY.

Query Match 50.0%; Score 41; DB 1; Length 402;
 Best Local Similarity 47.4%; Pred. No. 11;
 Matches 9; Conservative 1; Mismatches 1; Indels 8;
 Gaps 1;

3 WYASRG-----IRPGV 13
 ||||| :||| |

91 WYAPRQLSRAETKPGV 109
 ||||| :||| |

RESULT 7
 RECJ_ERWCH
 ID RECJ_ERWCH STANDARD; PRT; 575 AA.
 AC P39633; Q41007;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Single-stranded-DNA-specific exonuclease recj (EC 3.1.-.-).
 GN RECJ
 OS Erwinia chrysanthemi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=556;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RA Lovett S.T.; Itohaya M.; Sutera V.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases
 [2]
 RP SEQUENCE OF 1-100 FROM N.A.
 RN STRAN=3937;
 RC MEDLINE=94222048; PubMed=8168497;
 RX Shevchik V.B.; Condeine G.; Robert-Baudouy J.;
 RT "Characterization of Dsb_c, a periplasmic protein of Erwinia
 chrysanthemi and Escherichia coli with disulfide isomerase
 activity";
 RL EMBO J. 13:2007-2012 (1994).
 CC -!- FUNCTION: SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE. REQUIRED FOR
 MANY TYPES OF RECOMBINATIONAL EVENTS, ALTHOUGH THE STRINGENCY OF
 THE REQUIREMENT FOR RECJ APPEARS TO VARY WITH THE TYPE OF
 RECOMBINATIONAL EVENT. MONITORED AND THE OTHER RECOMBINATION GENE
 PRODUCTS WHICH ARE AVAILABLE (BY SIMILARITY).
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 CC -----
 CC DR EMBL: U57563; AAB02611; -.
 CC DR EMBL: X76587; CAA54109; -.
 CC DR InterPro; IPR03156; DHEA1.
 CC DR InterPro; IPR01667; Pposterase.
 CC DR InterPro; IPR04610; RecJ.
 CC DR Pfam: PF01368; DHH; 1.
 CC DR Ptam: PF02272; DHH1; 1.
 CC DR TIGR00644; recJ; 1.
 CC KW Hydrolase; Nuclease; Exonuclease.
 CC FT MNVVTQ -> MLLPN (IN REF. 2).
 CC FT CONFLICT 1 6 R -> G (IN REF. 2).
 CC FT CONFLICT 83 83 R -> H (IN REF. 2).
 CC FT CONFLICT 100 100 R -> H (IN REF. 2).
 CC SEQUENCE 575 AA; 4D06A037DFD5DBE4 CRCC4;
 SQ -----
 Query Match 48.8%; Score 40; DB 1; Length 575;
 Best Local Similarity 55.6%; Pred. No. 23;
 Matches 5; Conservative 2; Mismatches 2; Indels 0;
 Gaps 0;

1 CAYWARGI 9
 ||||| :||| |

208 CGWFAERGL 216
 DR -----
 DR EMBL: A1-939122; CAC05901; 1; -.
 DR HAMAP; MR_00378; /; 1.
 DR InterPro; IPR010375; /; 1.
 DR InterPro; IPR004365; tRNA_anti.
 DR Pfam; PF022601; Exonuc_VII_L.
 DR Pfam; PF01336; tRNA_anti; 1.
 DR TIGRFAMS; TIGR0023; xeaA; 1.
 KW Hydrolase; Nuclease; Exonuclease; Complete proteome.
 SEQUENCE 402 AA; 438882 MW; 145923A8372B4E08 CRCC4;
 SQ -----

RESULT 8
 ATPU_BOAST STANDARD PRT; 580 AA.
 ID P21115; P21115;
 AC P22136; P21115;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-1994 (Rel. 43, Last annotation update)
 DE ATP13 Protein, mitochondrial precursor.
 DE Eukaryota; Fungi; Ascomycota; Saccharomycetes;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Saccharomyces; Saccharomycetales; Saccharomycetes;
 OX NCBI_TaxID:4932;
 RN [1]
 SEQUENCE FROM N.A.; PubMed=18250655;
 RXN
 RA ACKERMAN, S.H.; GELLEFORS, P.; DOUGLAS, M.G.; TZAGOLOFF, A.;
 RT "ATP13, a nuclear gene of Saccharomyces cerevisiae essential for the
 expression of subunit 9 of the mitochondrial ATPase.";
 RL FEBS Lett. 278:234-238(1991).
 RN [2]
 SEQUENCE FROM N.A.;
 MEDLINE=92035073; PubMed=7118609;
 RA PAYNE, M.J.; FINNEGAN, P.M.; KERAMIDARI, E.; LUKINS, H.B.;
 RT "Characterization of a yeast nuclear gene, ARP2, required for
 accumulation of mitochondrial mRNA encoding subunit 9 of the ATP
 synthase.";
 RT Curr. Genet. 20:53-61(1991).
 RN [3]
 SEQUENCE FROM N.A.;
 STRAINS=S288C / AB972;
 RXN
 RA BOWMAN, S.; CHURCHER, C.M.; BADCOCK, K.; BROWN, D.; CHILLINGWORTH, T.;
 RA CONNOR, R.; DEDMAN, K.; DEVLIN, K.; GENTLES, S.; HAMILIN, N.; HUNT, S.;
 RA JAGELS, K.; LY, G.; MOLE, S.; ODELL, C.; PEARSON, D.; RAJANDREAM, M.A.;
 RA RICE, P.; SKELTON, J.; WALSH, S.; WHITEHEAD, S.; BARRELL, B.G.;
 RT XIII.";
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT VIII.";
 RN [4]
 SEQUENCE OF 1-108 FROM N.A.;
 STRAINS=S288C / YPH1;
 MEDLINE=95042750; PubMed=7954819;
 RA ASTROM, S.U.; BYSTREOM, A.S.;
 RT "Rit1, a tRNA backbone-modifying enzyme that mediates initiator and
 elongator tRNA discrimination.";
 RL Cell 79:535-546 (1994).
 CC -|- FUNCTION: Essential for the expression of subunit 9 of the
 CC mitochondrial ATPase.
 CC -|- SUBCELLULAR LOCATION: Mitochondrial.
 CC -|- MISCELLANEOUS: Mutations in ATP13 result in respiratory
 CC deficiency.
 CC -|- CAUTION: Ref.1 sequence differs from that shown from position 363
 CC onward and is shorter (372 AA) due to a frameshift.
 CC
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 CC
 DR EMBL; X556215; CAA39672.2; ALT_FRAME.
 DR EMBL; M98860; AA34412.1; -.
 DR EMBL; X49704; CAB89780.1; -.
 DR PIR; S80795; CAA56771.1; -.
 DR PIR; S8589; S54389.
 DR SED; S0004895; ARP2.
 KW Mitochondrion; Transit peptide.
 FT TRANSIT 1 25 MITOCHONDRION (OR 28) (POTENTIAL).
 FT CHAIN 26 580 ATP13 PROTEIN.

RESULT 9
 REC2_HAELN STANDARD PRT; 788 AA.
 ID REC2_HAELN
 AC P4408;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Recombination protein 2.
 DE REC2 OR REC-2 OR H10061.
 GN Haemophilus influenzae.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus; Haemophilus; Pasteurellales;
 OC NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=RG / KW20 / ATCC 51907;
 RXN
 RA MEDLINE=94341577; PubMed=8063112;
 RA Clifton, S.W.; McCarthy, D.; Roe, B.A.;
 RT "Sequence of the rec-2 locus of Haemophilus influenzae: homologies to
 RT comc-ORF3 of *Bacillus subtilis* and msBA of *Escherichia coli*.";
 RL Gene 146:95-100 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RG / KW20 / ATCC 51907;
 RXN
 RA MEDLINE=95350630; PubMed=7542800;
 RA Fleschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.;
 RA Keravage, A.R.; Bult, C.J.; Doughty, B.A.; Merrick, J.M.;
 RA McKenney, K.; Sutton, G.; Bilt, J.-F.; Tomb, J.-F.; Doughty, B.A.; Merrick, J.M.;
 RA Scott, J.D.; Shirley, R.; Liu, L.-I.; Glodek, A.; Kelley, J.M.;
 RA Weidman, J.F.; Phillips, B.; Spriggs, T.; Hedblom, E.; Cotton, M.D.;
 RA Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.;
 RA Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Gogebagen, N.S.M.;
 RA Gneim, C.L.; McDonald, L.A.; Small, R.V.; Fraser, C.M.; Smith, H.O.;
 RA Venter, J.C.;
 RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*
 RT Rd.;
 RL Science 269:496-512 (1995).
 CC -|- FUNCTION: Might contribute to transformation as a member of a
 CC membrane-bound pore complex at the base of the transformosome. It
 CC could directly interact with transforming DNA during translocation
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC -|- SIMILARITY: TO B.SUBTILIS COMEC, N.GONCRHOEAE COMA, AND E.COLI
 CC
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 CC
 DR EMBL; L20805; AAC13733.1; -.
 DR EMBL; U32691; AAC21739.1; -.
 DR PIR; 164045; 164045.
 DR TIGR; H10061; -.
 DR InterPro; IPR01279; Blaetmase-like.
 DR InterPro; IPR004477; ComEC_N-term.

DR InterPro; IPRO004797; ComEC_Fec2.
 DR Pfam; PF03753; Competence; 1.
 DR Pfam; PF00753; LacCammase_B; 1.
 DR TIGRFAMS; TIGR00360; ComEC_Nterm; 1.
 DR TIGRFAMS; TIGR0361; ComEC_Rec2; 1.
 Competence; Transport; Inner membrane; Transmembrane;
 KW Complete proteome;
 FT TRANSMEM 3 23 POTENTIAL.
 FT TRANSMEM 27 47 POTENTIAL.
 FT TRANSMEM 51 71 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 263 283 POTENTIAL.
 FT TRANSMEM 313 333 POTENTIAL.
 FT TRANSMEM 367 387 POTENTIAL.
 FT TRANSMEM 401 421 POTENTIAL.
 FT TRANSMEM 434 454 POTENTIAL.
 FT TRANSMEM 456 476 POTENTIAL.
 FT TRANSMEM 508 528 POTENTIAL.
 FT TRANSMEM 748 788 POTENTIAL.
 FT TRANSMEM 748 788 CONFLICT;
 FT SEQUENCE 788 AA; 89355 MW; F31104595CB4E47A CRCC4;
 SQ Query Match 3 WYASRGIRPVG 13
 Best Local Similarity 48.8%; Score 40; DB 1; Length 788;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 DB 156 WYFSKGITAVG 166
 RESULT 11
 EX7L_COREF ID EX7L_COREF STANDARD; PRT; 413 AA.
 AC Q8F0B1;
 DT 10-Oct-2003 (Rel. 42, Created)
 DT 10-Oct-2003 (Rel. 42, Last sequence update)
 DE Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6).
 GN XSEA OR CB1078.
 OS Corynebacterium efficiens.
 OB Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 NCBI_TaxID=152794;
 RN [1]_
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y5-314 / AJ_12310 / DSM 44549 / JCM 11189;
 RX MEDLINE=22723752; PubMed=12840036;
 RA Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
 RA Sugimoto S., Matsui K., Yamagishi A., Rikuchi H., Ikeo K.,
 RA Gojobori T.;
 RA RT "Comparative complete genome sequence analysis of the amino acid
 RT replacements responsible for the thermostability of Corynebacterium
 RT efficiens";
 RL Genome Res. 13:1572-1579 (2003).
 CC -!- FUNCTION: Bidirectional degrades single-stranded DNA into large
 CC acid-insoluble oligonucleotides, which are then degraded further
 CC into small acid-soluble oligonucleotides (By similarity).
 CC -!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5' to 3' -
 CC or 3' - to 5' - direction to yield nucleic 5'-phosphates.
 CC -!- SUBUNIT: Heterooligomer composed of large and small subunits (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the xseA family.
 CC
 RX MEDLINE=21173198; PubMed=11289647;
 RA Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 RA Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]_
 SEQUENCE FROM N.A.
 STRAIN=ATCC 19089 / CB15;
 RC MEDIUM=11289647;
 RA Nelson W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka T., Nelson W.C., Nelson A., Stepanov C., Phadke N.D., Ely B.,
 RA DeBoe R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kollaray J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salberberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
 CC -!- FUNCTION: This enzyme may play a significant role in processes
 CC leading to recovery from mutagenesis and/or cell death by
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of DNA containing ring-opened N(7)-
 CC methylguanine residues, releasing 2,6-diamino-4-hydroxy-5-(N-
 CC formamido)pyrimidine.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SIMILARITY: Belongs to the FPG family.
 CC
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 CC
 EMBL; AP005217; BAC17888; 1; ALT_INIT.
 DR HAMAP; MF 00378; 1.
 DR InterPro; IPR003753; Exonuc_VII_L.

DR	InterPro; IPR00994; Nucleic_acid_OB.
DR	PFam; PF0201; Exonuc VII_L_1.
DR	TIGRFAMS; TIGR00237; Xsea_1.
KW	Hydrolase; Nuclease; Exonuclease; Complete proteome.
SEQUENCE	413 AA; 45171 MW; D3BBD96B7C6BE5D CRC64;
Query Match	47.6%; Score 39; DB 1; Length 413;
Best Local Similarity	50.0%; Pred. No. 25;
Matches	10; Conservative 1; Mismatches 1; Indels 8; Gaps 1;
Qy	2 AWYASRG-----IRPVG 13
Db	91 AFYAGRSSFSFLWTTDIRPVG 110
RESULT 12	
ID	EX7L_CORG1
ID	EX7L_CORG1 STANDARD; PRT; 417 AA.
QNRM3;	
AC	P23832;
DT	01-NOV-1991 (Rel. 20, Created)
DT	01-NOV-1991 (Rel. 20, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	SAMB protein.
GN	SAMB_SALTY STANDARD; PRT; 424 AA.
OS	Salmonella typhimurium.
OG	Plasmid 60-mDa cryptic.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Salmonella.
NCBI_TaxID	602;
RN	SEQUENCE FROM N.A.
RP	STRAIN=ET2;
RC	Medline:91123176; PubMed=1991707;
RX	Nohmi T.; Hakura A.; Nakai Y.; Watanabe M.; Murayama S.Y.;
RA	Sotuni T.;
RA	"Salmonella typhimurium has two homologous but different umuDC operons cloning of a new umuDC-like operon (samAB) present in a 60-megadalton cryptic plasmid of <i>S. typhimurium</i> ."
RT	J. Bacteriol. 173:1051-1063 (1991).
CC	- - FUNCTION: Involved in UV protection and mutagenesis.
CC	- - SIMILARITY: Belongs to the DNA polymerase type-Y family.
CC	- - SIMILARITY: Contains 1 umuC domain.
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CC	EMBL; D90202; BRA14226.1;
CC	DR PIR; BB8176; B38176.
CC	DR HANAP; MF_0113; atypical; 1.
CC	DR InterPro; IPR00126; UMUC_like.
CC	DR Pfam; PF00817; INS; 1.
CC	DR PROSITE; PSS01173; JUMC; 1.
CC	DR Plasmid; SOS mutagenesis; DNA repair.
CC	FT DOMAIN 2 189 UMUC.
CC	SEQUENCE 424 AA; PP8C47476CC58A2B CRC64;
CC	Query Match 47.6%; Score 39; DB 1; Length 424;
CC	Best Local Similarity 56.7%; Pred. No. 25;
CC	Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy	3 WYASRGIRP 11
Db	390 WFAGRGIAAP 398
RESULT 14	
ID	GLPT_ECOLI
ID	GLPT_ECOLI STANDARD; PRT; 452 AA.
AC	P05194;
AC	01-AUG-1988 (Rel. 08, Created)
DT	01-AUG-1988 (Rel. 08, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Glycerol-3-phosphate transporter (G-3-P transporter) (G-3-P permease).
GN	Escherichia coli.
RN	SEQUENCE FROM N.A.
RC	STRAIN=K12;
RC	Medline:88201663; PubMed=3329281;
RA	Eiglewe K.; Boos W.; Cole S.;
RA	"Nucleotide sequence and transcriptional startpoint of the glpt gene
RESULT 13	
SAMR_SALTY	SEQUENCE FROM N.A.
STRAIN	OR B2240.
OS	Escherichia coli.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Escherichia.
NCBI_TaxID	562;
RN	SEQUENCE FROM N.A.
RC	STRAIN=K12;
RC	Medline:88201663; PubMed=3329281;
RA	Eiglewe K.; Boos W.; Cole S.;
RA	"Nucleotide sequence and transcriptional startpoint of the glpt gene
RESULT 13	
SAMR_SALTY	SEQUENCE FROM N.A.
STRAIN	OR B2240.
OS	Escherichia coli.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Escherichia.
NCBI_TaxID	562;
RN	SEQUENCE FROM N.A.
RC	STRAIN=K12;
RC	Medline:88201663; PubMed=3329281;
RA	Eiglewe K.; Boos W.; Cole S.;
RA	"Nucleotide sequence and transcriptional startpoint of the glpt gene
RESULT 13	
SAMR_SALTY	SEQUENCE FROM N.A.
STRAIN	OR B2240.
OS	Escherichia coli.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Escherichia.
NCBI_TaxID	562;
RN	SEQUENCE FROM N.A.
RC	STRAIN=K12;
RC	Medline:88201663; PubMed=3329281;
RA	Eiglewe K.; Boos W.; Cole S.;
RA	"Nucleotide sequence and transcriptional startpoint of the glpt gene

of *Escherichia coli*: extensive sequence homology of the glycerol-3-phosphate transport protein with components of the hexose-6-phosphate transport system." *J Mol. Microbiol.* 1:251-258 (1987).

[2] SEQUENCE FROM N.A.

STRAIN=K12 / MG1655; PubMed=9278503; MEDLINE=97146617; PubMed=9205937; MEDLINE=97349980; PubMed=9205937;

BLATTNER P.R., Plunkett G. III., Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Maur B., Shao Y.;

"The complete genome sequence of *Escherichia coli* K-12." *Science* 277:1433-1474 (1997).

[3] SEQUENCE FROM N.A.

STRAIN=K12; PubMed=9205937; MEDLINE=97349980; PubMed=9205937;

Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Makino K., Miki T., Mitsuhashi N., Itoh T., Kimura S., Kitagawa M., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saico N., Sampei G., Satoch Y., Sivarsundaram S., Tagami H., Takashashi H., Takeda J., Takedo K., Uehara K., Wada C., Yamazaki S., Horiuchi T.

"Construction of a contiguous 874-kb sequence of the *Escherichia coli* K12 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features." *J. DNA Res.* 4:91-113 (1997).

RN [4]
 RP TOPOLOGY.
 RP MEDLINE=83039254; PubMed=3141744;
 RX
 RA Goett P.; Boos W.;
 RT "the transmembrane topology of the sn-glycerol-3-phosphate permease of
 Escherichia coli analysed by phoA and lacZ protein fusions.";
 RT Mol. Microbiol. 2:655-663 (1988).
 RL 1- FUNCTION: Responsible for glycerol-3-phosphate uptake.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -1- SIMILARITY: Belongs to the major facilitator (MFS) superfamily.
 CC SLC37A family.
 CC

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CCR	EMBL: Y00536; CAA68598.1; -.		
EMBL: DR	AE003314; AAC75300.1; -.		
EMBL: DR	D90855; BAA16059.1; -.		
PIR: DR	S00868; JNECGT.		
EcoGene: DR	EG1001; G1PT.		
InterPro: DR	IPR005267; G1P transporter.		
InterPro: DR	IPR000849; G1P transporter.		
InterPro: DR	IPR007114; MFS transporter.		
TIGRFAMS: DR	TIGR000881; 2AC04. 1.		
TIGRFAMS: DR	TIGR00712; G1PT; 1.		
PROSITE: DR	PS00424; GLPT; 1.		
PROSITE: DR	PS505050; MFS; 1.		
KW	Glycerol metabolism; Transmembrane; Inner membrane; Transport; Complete processome.		
KW	DOMAIN 1 27 CYTOPLASMIC (PROBABLE).		
KW	DOMAIN 28 44 1 (PROBABLE).		
KW	TRANSMEM 45 64 1 (PROBABLE).		
KW	DOMAIN 65 87 2 (PROBABLE).		
KW	TRANSMEM 88 95 2 (PROBABLE).		
KW	DOMAIN 96 113 3 (PROBABLE).		
KW	TRANSMEM 114 119 4 (PROBABLE).		
KW	DOMAIN 120 136 4 (PROBABLE).		
KW	TRANSMEM 137 169 5 (PROBABLE).		
KW	DOMAIN 170 184 5 (PROBABLE).		
KW	TRANSMEM 176 190 6 (PROBABLE).		

RESULT 19	CBPB_BOVIN	STANDARD	PRT;	306 AA.
STRAIN2_PARTE	STANDARD;			
ID : CAL2_PARTE				
AC Q94715;				
DT 28-FEB-2003 (Rel. 41, Created)				
DT 28-FEB-2003 (Rel. 41, Last sequence update)				
DT 28-FEB-2003 (Rel. 41, Last annotation update)				
DE Putative cathepsin L2 (EC 3.4.22.15) (Fragment).				
CS Paramecium tetraurelia.				
OC Alveolata; Ciliophora; Oligohymenophorea; Peniculida;				
NCBI_TaxID:5988;				
OX				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=Stock 51;				
RX MEDLINE=1624439; PubMed=865938;				
RA Voelker H., Kurz U., Linder J., Klunpp S., Gnau V., Jung G.,				
RA Schulte J.E.;				
RT "Cathepsin L is an intracellular and extracellular Protease in				
RT Paramecium tetraurelia: Purification, cloning, sequencing and specific				
RT inhibition by its expressed propeptide.";				
RL Bur. J. Biochem. 238:198-206(1996).				
CC -!- FUNCTION: May be involved in extracellular digestion.				
CC -!- CATALYTIC ACTIVITY: Specificity close to that of papain. As				
CC compared to cathepsin B, cathepsin L exhibits higher activity				
CC towards protein substrates, but has little activity on Z-Arg-Arg-				
CC NH ₂ and no peptidyl-dipeptidase activity.				
CC -!- SUBCELLULAR LOCATION: Secreted.				
CC -!- SIMILARITY: Belongs to Peptidase family Cl.				
CC -!- CAUTION: This protein may be non-functional as it lacks the				
CC cysteine active site residue which is replaced by Gly-118.				
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CC -!- EMBL: X91756; CA62871.1; -.				
DR S68784; S68784.				
DR HSSP: Q09111; 1F00.				
DR InterPro; IPR000668; Peptidase_C1.				
DR InterPro; IPR000669; Sprote_acsite.				
DR Pfam: PF00112; Peptidase_C1; 1.				
DR ProdDom: PD000158; Peptidase_C1; 1.				
DR SMART; SM00645; Pept_C1; 1.				
DR PROSITE; PS00640; THIOL PROTEASE ASN FALSE NEG.				
DR PROSITE; PS00139; THIOL PROTEASE CYS FALSE NEG.				
DR PROSITE; PS00639; THIOL PROTEASE HIS FALSE NEG.				
KW Hydrolase; Thiol protease.				
FT NON_TER 1 1				
FT PROTEP <1 ?				
FT CHAIN ?				
FT ACT_SITE 118 118				
FT ACT_SITE 247 247				
FT ACT_SITE 264 264				
FT DISULFID 115 156				
FT DISULFID 240 284				
SQ SEQUENCE 294 AA; 33627 MW; 6FD688A0176BEC51 CRC64;				
Query Match 46.3%; Score 38; DB 1; Length 294;				
Best Local Similarity 54.5%; Pred. No. 27;				
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;				
QY 2 AWYASRGIRPV 12				
DB 129 AWYAIRGQKI 139				
RESULT 20				
CBPB_BOVIN				

RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002). [4]	ID ENO_MYCPU STANDARD; PRT; 456 AA.
RT	"Purification and properties of five different forms of human procarboxypeptidases"; R. J. Biochem. 179:609-616 (1989).	AC Q98550; Rel. 41, Created
RL	CC -I- CATALYTIC ACTIVITY: Peptidyl-L-lysine (or L-arginine) + H(2)O = peptide + L-lysine (or L-arginine).	DT 28-FEB-2003 (Rel. 41, Last sequence update)
RN	CC -I- TISSUE SPECIFICITY: Pancreas;	DT 28-FEB-2003 (Rel. 41, Last annotation update)
RP	CC MEDLINE=99153096; PubMed=2920728; Pascual R., Burgos F.J., Scriano F., Mendez E., Aviles F.X.; "Purification and properties of five different forms of human procarboxypeptidases"; R. J. Biochem. 179:609-616 (1989).	DB Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
RX	CC TISSUE=Pancreas;	GN ENO OR MYPU 5180.
RA	CC Mycoplasma pulmonis.	OS Mycoplasma pulmonis.
RT	CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.	OC
RT	CC NCBI_TaxID=2107;	OX
RT	CC RN [1] _	RP SEQUENCE FROM N.A.
RL	CC STRAIN=DAB CTPP;	RC MEDLINE=21267165; PubMed=11353084;
RN	CC CHABAUD I., HEILIG R., PERRIS S., BARBE V., SAMSON D., GALLISSON F., BLANCHARD A.; "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis"; Nucleic Acids Res. 29:2145-2153 (2001).	RA Moser I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C., H(2)O.
RP	CC -I- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + the dimer. (By similarity).	RA -I- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer. (By similarity).
RX	CC -I- SUBUNIT: Homodimer (By similarity).	CC -I- PATHWAY: Glycolysis.
RA	CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	CC -I- SIMILARITY: Belongs to the emolase family.
RT	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).
RT	CC EMBL; M81057; AA66973.1; -.	CC EMBL; AA45564; CRC13691.1; -.
EMBL	CC EMBL; AA724866; CAA12163.1; -.	DR PIR; F90576; F90576.
PDB	CC DR PDB; 1KWM; AAH15338.1; -.	DR MYNIList; MYPU 5180; -.
1KWM	CC DR PDB; 1KWM; 28-AUG-02.	DR HAPIP; MF_00318; -.
MEROPS	CC DR MEROPS; M14_003; -.	DR InterPro; IPR000941; Emolase.
CPB1	CC DR CPB1; HGNC-2299; CPB1.	DR PFam; PF001113; emolase; 1.
Gene	CC DR MIM; 114852; -.	DR PFam; PF03952; emolase; N; 1.
GO	CC DR GO; GO:0004180; F:carboxypeptidase activity; TAS.	DR PRINTS; PR00148; ENOLASE.
InterPro	CC DR InterPro; IPR0003146; Peptidase_M14.	DR PRODom; PD000902; Emolase; 1.
Protein	CC DR InterPro; IPR000834; Peptidase_M14.	DR TIGRFAMS; TIGR01060; eno; 1.
InterPro	CC DR InterPro; IPR000320; Protease_inhib.	DR PROSITE; PS00164; ENOLASE; 1.
InterPro	CC DR InterPro; IPR02244; Protop; M14; 1.	KW Lyase; Glycolysis; Magnesium; Complete proteome.
PFam	CC DR PFam; PF00246; ZincCarboxypeptidase; 1.	FT ACT_SITE 159 159 BY SIMILARITY.
PFam	CC DR SMART; SM00631; Zinc Peptidase.	FT METAL 250 250 MAGNESIUM (BY SIMILARITY).
PFam	CC DR PROSITE; PS00132; CARBOXYPEPTIDASE_ZN_1; 1.	FT DISULFID 312 312 MAGNESIUM (BY SIMILARITY).
PFam	CC DR PROSITE; PS00133; CARBOXYPEPTIDASE_ZN_2; 1.	FT METAL 339 339 MAGNESIUM (BY SIMILARITY).
KW	CC Hydrolease; Carboxypeptidase; Metalloprotease; Zinc; Zymogen; Signal; 3D-structure.	FT SEQUENCE 456 AA; 4987 MW; 330300BFF0FDE2A2 CRC64;
KW	CC SIGNAL 1 15 ACTIVATION PEPTIDE.	Query Match Score 38; DB 1; Length 456;
PROPEP	CC PROPEP 16 110 CARBOXYPEPTIDASE_B.	Best Local Similarity 62.5%; Pred: No; 41;
FT	CC CHAIN 111 417 BY SIMILARITY.	Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
FT	CC METAL 176 176 ZINC (BY SIMILARITY).	FT
FT	CC METAL 179 179 ZINC (BY SIMILARITY).	FT
FT	CC METAL 304 304 ZINC (BY SIMILARITY).	FT
FT	CC ACT_SITE 378 378 ZINCOPHILE (BY SIMILARITY).	FT
FT	CC DISULFID 173 186 BY SIMILARITY.	FT
FT	CC PROPEP 245 268 BY SIMILARITY.	FT
FT	CC DISULFID 259 273 BY SIMILARITY.	FT
FT	CC CONFLICT 16 16 H -> A (IN REF. 1; AA SEQUENCE).	FT
FT	CC CONFLICT 17 17 H -> Q (IN REF. 1; AA SEQUENCE).	FT
FT	CC CONFLICT 37 37 H -> Q (IN REF. 4).	FT
FT	CC CONFLICT 208 208 D -> N (IN REF. 2).	FT
FT	CC CONFLICT 245 245 MISSING (IN REF. 1).	FT
SEQUENCE	CC SEQUENCE 417 AA; 47367 MW; BBBB998B27F5DSAF9 CRC64;	FT
SEQUENCE	CC Best Local Similarity 35.7%; Pred: No; 37; Indels 0; Gaps 0;	FT
Matches	CC Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;	FT
5;	5;	FT
QY	1 CAYASRGIRPVGR 14	RESULT 24
Db	186 CWFVRAVTRGR 199	SM6C_HUMAN STANDARD; PRT; 930 AA.
Db	10-OCT-2003 (Rel. 40, Created)	ID SM6C_HUMAN STANDARD; PRT; 930 AA.
Db	28-FEB-2003 (Rel. 41, Last sequence update)	AC Q9HAT2; Q8WXT8; Q8WUX0; Q96JF8;
Db	10-OCT-2003 (Rel. 42, Last annotation update)	DT Semaphorin 6C precursor (Semaphorin Y) (Sema Y).
Db	DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).	DE

GN SEMA6C OR SEMA7A OR KIAA1869.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RA Kimura T., Ishida H.;
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Brain;
 RA Nagase T., Nakajima D., Kikuno R., Ohara O.;
 RA "Prediction of the coding sequences of unidentified human genes. XX.
 RT The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro.";
 RT Res 8:85-95(2001).
 CC -!- FUNCTION: May be a stop signal for the dorsal root ganglion
 neurons in their target areas, and possibly also for other
 neurons. May also be involved in the maintenance and remodeling of
 neuronal connections (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Short 1;
 CC Name=2; Synonyms=Short 2;
 CC IsoId=Q9H3T2; Sequence=Displayed;
 CC IsoId=Q9H3T2; Sequence=vSP_00046; vSP_006047;
 CC Name=3; Synonyms=Long;
 CC IsoId=Q9H3T2; Sequence=vSP_00047;
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.

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CC EMBL; AB024434; BA220670; -;
 DR EMBL; AF339152; AAL72098; -;
 DR EMBL; AF339153; AAL72099; -;
 DR EMBL; AF339154; AAL72100; -;
 DR EMBL; AB058772; BA847498; ALT_INIT.
 DR Genew; HGNC:1040; SEMAC.
 DR InterPro; IPR003659; Plexin-like.
 DR Pfam; PF01403; Sema_1.
 DR SMART; SM00630; Sema_1.
 DR SMART; SM00631; Sema_1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 930 SEMAPHORIN_6C.
 FT DOMAIN 25 604 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 605 625 CYTOSMIC (POTENTIAL).
 FT DOMAIN 626 540 SEMA.
 FT DOMAIN 627 667 POLY-PRO.
 FT DOMAIN 752 755 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 437 99682 MW; 8AF8814ADBCH4C88 CRC64;
 SQ [3]

Query Match 46.3%; Score 38; DB 1; Length 930;
 Best Local Similarity 62.5%; Pred. No. 82;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 25
 BCAT CAEEL STANDARD; PRT; 415 AA.
 ID BCAT CAEEL
 AC P54638;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Branched-chain amino acid aminotransferase, cytosolic (EC 2.6.1.42)
 DE (BCAT) (ECA39 protein).
 GN ECA-39 OR ECA39 OR K02AA4.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Pelerodinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN_Bristol_N2;
 RA McMurray A.A.;
 RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE OF 21-398 FROM N.A.
 RP MEDLINE=96293440; PubMed=8692959;
 RX Schudliner O., Eden A., Ben-Yosef T., Yanuka C., Simchen G.,
 RA Benvenisty N.;
 RT "ECA39, a conserved gene regulated by c-Myc in mice, is involved in
 G1/S cell cycle regulation in yeast.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7143-7148 (1996).
 CC -!- FUNCTION: Catalyzes the first reaction in the catabolism of the
 CC essential branched chain amino acids leucine, isoleucine, and
 CC valine.
 CC -!- CATALYTIC ACTIVITY: L-leucine + 2-oxoglutarate = 4-methyl-1-2-
 CC oxopentanone + L-glutamate.
 CC -!- COFACTOR: Pyridoxal phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasm.
 CC -!- SIMILARITY: Belongs to class-IV of pyridoxal-phosphate-dependent
 CC aminotransferases.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; Z67883; QAA91805; 1;
 DR EMBL; U21550; AAC47236; 1;
 DR PIR; T23215; T23215;
 DR HSSP; P00510; 1A3G.
 DR WormPP; K02AA4.1; CB03457.
 DR InterPro; IPR01544; Aminotrans-IV.
 DR InterPro; IPR05786; Amino_trans-IV.
 DR Pfam; PF01063; aminotran_4; 1.
 DR Prodom; PDD01961; Aminotran_4; 1.

DR TIGERAMS; TIGR01123; ilvE_III; 1.
 DR PROSITE; PS00770; AA TRANSFER; CLASS 4; 1.
 KW Pyridoxal Aminotransferase; Branched-chain amino acid biosynthesis;
 PT BINDING 244 244 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 PT CONFLICT 86 86 D -> I (IN REF. 2).
 PT CONFLICT 118 118 F -> FS (IN REF. 2).
 PT CONFLICT 154 170 DEDSEEMINVTELLRL -> VFLRLGDDQCTYRLS (IN REF. 2).
 PT CONFLICT 391 397 MKFVNT -> RKLQHN (IN REF. 2).
 SQ SEQUENCE 415 AA; 47341 MW; AE216PC96223FB390 CRC64;
 Query Match 45.7%; Score 37.5; DB 1; Length 415;
 Best Local Similarity 44.4%; Pred. No. 46;
 Matches 8; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

Qy 1 CAWYASR-----IRPYG 13
 Db 83 CDWDAERGWHHPXLEPIG 100

RESULT 26
 ID R157_BOVIN STANDARD; PRT; 147 AA.
 AC Q28183_1
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Retina-specific 15.7 kDa protein.
 OS Bovinus (Bovine).
 EC Eukaryote; Mucocoe; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Bovidae; Bovinae; Bos.
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC TISSUE-Retina;
 RX MEDLINE=86581668; PubMed=2425311;

RA Nakagawa Y.; Kuo C.H.; Ishii K.; Shiosaka S.; Tohyama M.; Miki N.;
 RT "Cloning and characterization of a cDNA specific for bovine retina.";
 RL Neurosci. Res. 3:301-310 (1986).
 CC -1- TISSUE SPECIFICITY: Retina.
 CC SEQUENCE FROM N. A.

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DR PIR: T45978; T45978. 15658 MW; 1FED48788B39645 CRC64;

SQ SEQUENCE 147 AA; 15658 MW; 1FED48788B39645 CRC64;

Query Match 45.1%; Score 37; DB 1; Length 147;
 Best Local Similarity 71.4%; Pred. No. 20;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAWYASR 7
 Db 100 CSWFASR 106

RESULT 27
 ID Y064_TREPA STANDARD; PRT; 191 AA.
 AC 083103;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein TP0064.

CC GN TP0064.

OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 KW [1] _TaxID=160;
 RN SEQENCE FROM N. A.
 RP NCBINUM=Nichols;
 RC MEDLINE=9833270; PubMed=9665876;
 RA Fraser C.M.; Norris S.J.; Weinstock G.M.; White O.; Sutton G.G.;
 RA Dodson R.; Gwynn M.; Hickam B.K.; Clayton R.; Ketchum K.A.;
 RA Sodergren E.; Hardison R.; McLeod M.P.; Salzberg S.; Peterson J.J.;
 RA Khalak H.; Richardson D.; Howell J.K.; Chidambaram M.; Utterback T.;
 RA McDonald L.; Artiach C.; Cotton M.D.; Fujii C.; Garland S.;
 RA Hatch B.; Horst K.; Roberts K.; Sandusky M.; Weidman J.; Smith H.O.;
 RA Venter J.C.
 RA "Complete genome sequence of *Treponema pallidum*, the syphilis
 spirochete."; Science 281:375-388 (1998).
 CC
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CC

RESULT 28
 ID DAPP_CHLPE STANDARD; PRT; 257 AA.
 AC Q8RXX9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Diaminopimelate epimerase (EC 5.1.1.7) (DAP epimerase).
 GN DAPP OR CT2021;
 OS Chlorobium tepidum.
 CC Bacteria; Chlorobi; Chlorobi; Chlorobiaceae;
 OC Chlorobium.
 OC NCBITaxID=10977;
 RN SEQENCE FROM N. A.
 RP STRAIN=TLS / ATCC 49652 / DSM 12025;
 RC MEDLINE=2103685; PubMed=1203901;
 RA Eisen J.A.; Nelson K.E.; Paulsen I.T.; Heidelberg J.F.; Wu M.;
 RA Dodson R.J.; Deboy R.; Gwinn M.L.; Nelson W.C.; Haft D.H.;
 RA Hickey E.K.; Peterson J.D.; Durkin A.S.; Kolonay J.L.; Yang F.;
 RA Holt I.; Umayam L.A.; Mason T.; Brenner M.; Shoa T.P.; Parksey D.;
 RA Nierman W.C.; Feldblyum T.V.; Hansen C.L.; Craven M.B.; Radune D.;
 RA Vaishnavan J.; Khouri H.; White O.; Gruber T.M.; Ketchum K.A.;
 RA Venter J.C.; Tettelin H.; Bryant D.A.; Fraser C.M.;
 RT "The complete genome sequence of *Chlorobium tepidum* TLS, a
 RT photosynthetic, anaerobic, green-sulfur bacterium.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
 RL CC -! CATALYTIC ACTIVITY: LL-2,6-diaminohexanedioate = meso-
 CC CC -! PATHWAY: Biosynthesis of lysine from aspartate semialdehyde; sixth
 CC CC -! STEP.
 CC CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-1- SIMILARITY: Belongs to the diaminopimelate epimerase family.

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DR InterPro; IPR003006; Racem decarbox_C.
 DR InterPro; IPR001608; UPF0001.
 DR PF00042; Ala_racemase_C; 1.
 DR PF01168; Ala_racemase_N; 1.
 DR PRINTS; PRO0992; ALANINE_RACEMASE.
 DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
 KW Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis; Complete proteome.
 FT ACT_SITE 42 42 CATALYTIC BASE SPECIFIC TO D-ALANINE (BY SIMILARITY).
 FT ACT_SITE 257 257 CATALYTIC BASE SPECIFIC TO L-ALANINE (BY SIMILARITY).
 FT BINDING 42 42 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 397 AA; 43462 MW; 15996F5136A9C307 CRC64;
 Query Match 45.1%; Score 37; DB 1; Length 397;
 Best Local Similarity 60.0%; Pred. No. 54;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 WYASRGRPV 12
 Db 98 WTRSHGLIPV 107

RESULT 31
 SRP54_HALN1 STANDARD; PRT; 460 AA.
 AC Q9HMNF;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Signal recognition 54 kDa protein (SRP54).
 GN SRP54 OR VNG2459c.
 OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OC NCBI_TaxID=6409;-; RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2054483; PubMed=1101650;
 RA Ng W.V., Kennedy S.P., Mahaiares G.G., Berquist B., Pan M., Thorsson V., Sbrigno J., Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sbrigno J., Swartz D., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenberger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Fritas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebbhardt H., Low T.M., Liang P., Hood L., Dassarma S.; RT Genome sequence of Halobacterium species NRC-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
 CC 1- FUNCTION: Binds to the signal sequence of pressecretory protein when they emerge from the ribosomes (By similarity).
 CC 1- SUBUNIT: Archaeal signal recognition particle consists of a 7S RNA molecule of 300 nucleotides and two protein subunits: SRP54 and SRP19 (By similarity).
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC 1- DOMAIN: Has a two domain structure: the G-domain binds GTP; the M-domain binds the 7S RNA in presence of SRP19 and also binds the signal sequence (By similarity).
 CC 1- SIMILARITY: Belongs to the GTP-binding SRP family.

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CC DR EMBL; AB005125; AAG20536.; -.
 CC DR PIR; D84396; D84196.
 CC DR HSSP; C07347; 2FPH.
 CC DR HAMAP; MF_00306; -; 1.

DR InterPro; IPR00300; SRP54; FALSE NEG.
 DR Signal recognition particle; GTP-binding; RNA-binding; KW Complete proteome.
 KW Complete proteome.
 KW G-DOMAIN (BY SIMILARITY).
 FT DOMAIN 1 289 M-DOMAIN (BY SIMILARITY).
 FT NP_BIND 104 111 GTP (BY SIMILARITY).
 FT NP_BIND 184 188 GTP (BY SIMILARITY).
 FT NP_BIND 242 245 GTP (BY SIMILARITY).
 FT DOMAIN 449 459 POLY-GLY.
 SQ SEQUENCE 460 AA; 50149 MW; 8361B782E651352E CRC64;
 Query Match 45.1%; Score 37; DB 1; Length 460;
 Best Local Similarity 44.4%; Prod. No. 62;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WYASRGRPV 11
 Db 120 WFSKKGGLRP 128

RESULT 32
 SRP54_HALVO STANDARD; PRT; 465 AA.
 AC Q974_HALVO
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Signal recognition 54 kDa protein (SRP54).
 OS Halobacterium volcanii (Haloflexax volcanii).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Haloflexax.
 OX NCBI_TaxID=2446;
 OX

SEQUENCE FROM N.A. [1]
 RA Rose R.W., Pohlschroder M.;
 RA Rose R.W., Pohlschroder M.;
 RA Pohlschroder M.;
 RL FUNCTION: Binds to the signal sequence of pressecretory protein when they emerge from the ribosomes (By similarity).
 CC -1- SUBUNIT: Archaeal signal recognition particle consists of a 7S RNA molecule of 300 nucleotides and two protein subunits: SRP54 and SRP19 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- DOMAIN: Has a two domain structure: the G-domain binds GTP; the M-domain binds the 7S RNA in presence of SRP19 and also binds the signal sequence (By similarity).
 CC -1- SIMILARITY: Belongs to the GTP-binding SRP family.

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CC DR EMBL; AF95887; AAF93933.; -.
 CC DR HAMAP; MF_00306; -; 1.
 CC DR InterPro; IPR003593; AAA-ATPase.
 CC DR InterPro; IPR000897; SRP54.
 CC DR InterPro; IPR004125; SRP54_SPB.
 CC DR Pfam; PF0048; SRP54; 1.
 CC DR Pfam; PF00881; SRP54; 1.
 CC DR HSSP; C07347; 2FPH.
 CC DR HAMAP; MF_00306; -; 1.

GN	GNP1 OR KIAA0124.
DR	Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
FRW	SEQUENCE FROM N.A. TISSUE=Brain, Eye, Lymph, Muscle, and Pancreas;
DOMAIN	SEQUENCE FROM N.A. TISSUE=Brain, Eye, Lymph, Muscle, and Pancreas;
NP_BIND	SEQUENCE FROM N.A. TISSUE=Brain, Eye, Lymph, Muscle, and Pancreas;
NP_BIND	SEQUENCE FROM N.A. TISSUE=Brain, Eye, Lymph, Muscle, and Pancreas;
NP_BIND	SEQUENCE FROM N.A. TISSUE=Brain, Eye, Lymph, Muscle, and Pancreas;
SEQUENCE	SEQUENCE FROM N.A. TISSUE=Brain, Eye, Lymph, Muscle, and Pancreas;
Query Match	Score 37; DB 1; Length 465;
Best Local Similarity	44.4%; Prod. No. 62; Gaps 0;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	
Qy	3 WYASRGIRP 11
Ddb	120 WFSKGLRP 128
RESULT 33	
ID	NCNP_CCHFV
AC	P2317;
CC	STANDARD; PRT; 482 AA.
CC	01-AUG-1992 (Rel. 23, Created)
CC	01-AUG-1992 (Rel. 23, Last sequence update)
CC	01-JUL-1993 (Rel. 26, Last annotation update)
CC	"Comparison of the S RNA segments and nucleoprotein sequences of Nucleocapsid protein (Nucleoprotein)."
GN	"Crimean-Congo hemorrhagic fever virus (isolate C68031) (CCHFV). Viruses; ssRNA negative-strand viruses; Bunyaviridae; Nairovirus. NCP1_TaxID=11594;"
OC	SEQUENCE FROM N.A. MEDLINE=92351584; PubMed=1641991;
DR	Maxfield A.C., Nutall P.A.; "Comparison of the S RNA segments and nucleoprotein sequences of Crimean-Congo hemorrhagic fever, Hazara, and Dugbe viruses."; Virology 189:795-799(1992).
CC	-1 - SUBCELLULAR LOCATION: Internal protein of virus particle.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; MB6625; AAA42888; 1; -.
DR	PIR; B42990; VHVUCH
DR	InterPro; IPR03486; Nairo_nucleocap.
DR	ProDom; PD006459; Nairo_nucleocap; 1.
DR	Nucleocapsid RNA-binding.
SEQUENCE	Score 37; DB 1; Length 465;
Best Local Similarity	66.7%; Prod. No. 65; Gaps 0;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 CAWVSRGI 9
Ddb	80 CAWVSTGI 88
RESULT 34	
DR	DRP1_HUMAN
DR	STANDARD; PRT; 746 AA.
DR	Q14137; Q96926; Q9BSA7; Q9BYN0;
DR	01-NOV-1997 (Rel. 35, Created)
DR	28-FEB-2003 (Rel. 41, Last sequence update)
DR	10-OCT-2003 (Rel. 42, Last annotation update)
DR	Block of proliferation 1
DR	PROSITE; PS00320; WD40; 1.
DR	SMART; SM00510; AAH05160; 1; ALT_INIT.
DR	EMBL; BC001274; AAH07274; 1; ALT_INIT.
DR	EMBL; BC013787; AAH13787; 1; -.
DR	EMBL; BC033980; AAH13980; 1; -.
DR	EMBL; BC017674; AAH17674; 1; -.
DR	EMBL; D50914; BAA0973; 1; -.
DR	SWISS-2DPAGE; Q14137; HUMAN.
DR	Genew; HGNC:15519; BOP1.
DR	InterPro; IPR001680; WD40.
DR	Pfam; PF00400; WD40; 6.
DR	ProDom; PD000018; WD40; 1.
DR	SMART; SM00520; WD40; 7.
DR	PROSITE; PS00678; WD_REPEATS; 1; 1.
DR	PROSITE; PS50082; WD_REPEATS; 2; 2.
DR	PROSITE; PS50294; WD_REPEATS; REGION; 2.
KW	Nuclear protein; Repeat; WD Repeat.

FT REPEAT 411 450 WD 1.
 FT REPEAT 452 492 WD 2.
 FT REPEAT 532 576 WD 3.
 FT REPEAT 577 615 WD 4.
 FT REPEAT 618 657 WD 5.
 FT REPEAT 661 700 WD 6.
 FT REPEAT 716 745 WD 7.
 FT REPEAT 577 577 R -> H (IN REF. 2).
 SQ SEQUENCE 746 AA; 83629 MW; 49A9|BE2|B0EB3|DD CRC64;

Query Match 45.1%; Score 37; DB 1; Length 768;
 Best Local Similarity 75.0%; Prod. No. 1e+02;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAYWASERGIRPVG 13
 Db 620 CRKVSSLAVHPAG 632

RESULT 35
 METE_LACPL STANDARD; PRT; 768 AA.
 AC Q88X63; 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase
 DE (EC 2.1.14) (Methionine synthase, vitamin-B12 independent isozyme)
 DE (Cobalamin-independent methionine synthase).
 OS METE OR LP 1375.
 OC Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TAXID=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCINB_8826 / WCP51;
 RX MEDLINE=224B0296; PubMed=121566566;
 RA Kleerebezem M., Boekhorst J., van Kraanenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Piers M.W.E.J., Stieksma W., Klein Lankhorst R.M., Bron P.A.,
 RA Hoffer S.M., Nierop Groot M.N., Kerhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen R.J.
 RT "Complete genome sequence of Lactobacillus plantarum WCP51.";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).
 CC -!- FUNCTION: Catalyzes the transfer of a methyl group from 5-methyltetrahydrofolate to homocysteine resulting in methionine formation (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-homocysteine = tetrahydropteroyl-L-glutamate + L-methionine.
 CC -!- COFACTOR: Zinc; binds one ion per subunit (By similarity).
 CC -!- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
 CC -!- SIMILARITY: Belongs to the vitamin-B12 independent methionine synthase family.
 CC EMBL: AL935556; CAD63852.1; -.

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CC DR HAMAP; MF_00172; -; 1.
 CC DR InterPro; IPR002429; Methionine_synth.
 CC DR Pfam; PF01717; Methionine_Synth_1.
 CC KW Transfase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat; Complete proteome.
 CC FT METAL 650 650 ZINC (BY SIMILARITY).
 CC FT METAL 652 652 ZINC (BY SIMILARITY).
 CC FT METAL 735 735 ZINC (BY SIMILARITY).
 CC SEQUENCE 768 AA; 86432 MW; 477E4CE0C87ECE24 CRC64;

Query Match 45.1%; Score 37; DB 1; Length 768;
 Best Local Similarity 75.0%; Prod. No. 1e+02;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YASGIRP 11
 Db 521 YGSRGVRP 528

RESULT 36
 EPB_MOUSE STANDARD; PRT; 987 AA.
 AC P54761; Q60627;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-B receptor 4 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor MDK-2) (Developmental kinase 2) (Tyrosine kinase MDK-1).
 DE 1.
 DE EPB4 OR MDK2 OR MYK1 OR HTK.
 CN OS Mus musculus (Mouse).
 OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Murinae; Mus.
 OC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX OX NCBITaxonID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=BALB/C; TISSUE=Kidney;
 RX MEDLINE=16074837; PubMed=7478528;
 RA Ciossek T., Lerner M.M., Ullrich A.;
 RA "Cloning, characterization and differential expression of MDK2 and MDK5, two novel receptor tyrosine kinases of the eck/eph family.";
 RL Oncogene 11:2085-2095 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Lung;
 RX MEDLINE=04203677; PubMed=8152808;
 RA Andrees A.C., Reid H.H., Zurcher G., Blaschke R.J., Albrecht D.,
 RA Ziemiecki A.;
 RA "Expression of two novel eph-related receptor protein tyrosine kinases in mammary gland development and carcinogenesis.";
 RT RT Oncogene 9:1461-1467 (1994).
 RL "FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO EPHRIN-B2."
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: DEVELOPING CARDIOVASCULAR SYSTEM.
 CC -!- DEVELOPMENTAL STAGE: ABUNDANT EXPRESSION AT E16.5 IN VARIOUS ORGAN SYSTEMS, INCLUDING THYMUS, HEART, LUNGS AND KIDNEY, WHICH APPEARED TO BE ASSOCIATED WITH CELLS OF ENDOTHELIAL ORIGIN.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.

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CC DR EMBL; 249085; CAA89091; -.
 CC DR EMBL; U06834; AAA18591; -.
 CC DR PIR; I48652; I48652.
 CC DR PIR; I48653; I48653.
 CC DR HSSP; P23323; 1B4P.
 CC DR MGI; MGI-10477; Ephb4.
 CC DR InterPro; IPR006209; EGF-like.
 CC DR InterPro; IPR01050; Ephrin receptor.
 CC DR InterPro; IPR008957; FN_III-like.

DR	InterPro; IPR003961; FN III; subd.	DT	01-NOV-1997 (Rel. 35, Last sequence update)
DR	InterPro; IPR00972; Gal-bind like.	DT	01-NOV-1997 (Rel. 35, Last annotation update)
DR	InterPro; IPR007719; Prot_kinase.	DB	Putative short-chain type dehydrogenase/reductase Y4VI (EC 1.-.-.-).
DR	InterPro; IPR001650; SAM.	GN	Y4VI
DR	InterPro; IPR001245; Tyr_pk kinase.	OS	Rhizobium sp. (strain NGR234).
DR	InterPro; IPR008266; Tyr_pk kinase_AS.	OG	Plasmid sym NGR234a.
DR	Pfam; PF01404; Epiph_1bdc.	OC	Bacteria; Protoplastobacteria; Rhizobiales;
DR	Pfam; PF00041; Fn3; 2.	OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
DR	Pfam; PF00069; pk kinase; 1.	NCBI_TaxID	394.
DR	Pfam; PF00536; SAM; 1.	RN	
PRINTS	PRO0014; PTNPTPEIII.	RP	SEQUENCE FROM N.A.
PRINTS	PRO0014; TYRKTC; 1.	RX	Medline=97305956; PubMed=9163424;
PRINTS	PRO0109; TYRKINASE.	RA	Freiberg C.A., Ferret X., Broughton W.J., Rosenthal A.,
ProDom	PD001495; Ephrin receptor; 1.	RA	Broughton R., Bairach A.,
ProDom	PD000001; Prot_kinase; 1.	RA	Perret X.,
SMART	SM00615; EPH_1bdc; 1.	RT	"Molecular basis of symbiosis between Rhizobium and legumes.";
SMART	SM00060; Fn3; 2.	RL	Nature 387, 394-401(1997).
SMART	SM00454; SAM; 1.	RN	
SMART	SM0219; TYRKTC; 1.	RP	SEQUENCE FROM N.A.
PROSITE	PS01186; EGF; 2; UNKNOWN 1.	RX	Medline=98389014; PubMed=8795346;
PROSITE	PS00107; PROTEIN_KINASE_ATP; 1.	RA	Freiberg C., Ferret X., Broughton W.J., Rosenthal A.,
PROSITE	PS50011; PROTEIN_KINASE_DOM; 1.	RT	"Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
PROSITE	PS00109; PROTEIN_KINASE_TYR; 1.	RT	NGR234 using dye terminators and a thermostable 'sequenase' a
PROSITE	PS00790; RECEPTOR_TYR_KIN_V_1; 1.	RT	beginning";
PROSITE	PS00791; RECEPTOR_TYR_KIN_V_2; 1.	RL	Genome Res. 6:590-600(1996).
PROSITE	PS50105; SAM_DOMAIN; 1.	CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
KW	Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;	CC	(NSDR) FAMILY. CONTAINS TWO DOMAINS.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat.		CC	
PT	SIGNAL	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
PT	15	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
PT	CHAIN	CC	the European Bioinformatics Institute. There are no restrictions on its
PT	16	CC	use by non-profit institutions as long as its content is in no way
PT	539	CC	modified and this statement is not removed. Usage by and for commercial
PT	DOMAIN	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).
PT	16	CC	
PT	TRANSMEM	CC	
PT	540	CC	
PT	560	CC	
PT	DOMAIN	CC	
PT	561	CC	
PT	184	CC	
PT	320	CC	
PT	DOMAIN	CC	
PT	321	CC	
PT	429	CC	
PT	430	CC	
PT	528	CC	
PT	DOMAIN	CC	
PT	615	CC	
PT	899	CC	
PT	907	CC	
PT	971	CC	
PT	SITE	CC	
PT	985	CC	
PT	987	CC	
PT	NP BIND	CC	
PT	621	CC	
PT	629	CC	
PT	BINDING	CC	
PT	647	CC	
PT	740	CC	
PT	740	CC	
PT	MOD RES	CC	
PT	590	CC	
PT	590	CC	
PT	MOD RES	CC	
PT	596	CC	
PT	596	CC	
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	Multifunctional enzyme.
PT	ATP (BY SIMILARITY).	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	740	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	SAM.	FT	KW
PT	907	FT	Multifunctional enzyme.
PT	971	FT	DOMAIN 1 250
PT	SAM.	FT	DOMAIN 271 548
PT	985	FT	PF00106; adh_short; 2.
PT	987	FT	PROSITE; PRO0080; SURFAMILY.
PT	NP BIND	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	621	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	629	FT	KW
PT	BINDING	FT	Multifunctional enzyme.
PT	647	FT	DOMAIN 1 250
PT	740	FT	DOMAIN 271 548
PT	740	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT	PDZ-BINDING MOTIF (POTENTIAL).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PRO0080; SURFAMILY.
PT	ATP (BY SIMILARITY).	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	ATP (BY SIMILARITY).	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	ACT_SITE	FT	KW
PT	740	FT	Multifunctional enzyme.
PT	740	FT	DOMAIN 1 250
PT	ATP (BY SIMILARITY).	FT	DOMAIN 271 548
PT	ATP (BY SIMILARITY).	FT	PF00106; adh_short; 2.
PT	ACT_SITE	FT	PROSITE; PRO0080; SURFAMILY.
PT	740	FT	PROSITE; PS00061; ADH_SHORT; 1.
PT	MOD RES	FT	Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
PT	590	FT	KW
PT	596	FT	Multifunctional enzyme.
PT	596	FT	DOMAIN 1 250
PT			

OC T7-like viruses.
 OC NCBI_TAXID=10760;
 [1] SEQUENCE FROM N.A.
 RP MEDLINE=83241725; PubMed=6864790;
 RX Dunn J.J.; Studier F.W.;
 RA "Complete nucleotide sequence of bacteriophage T7 DNA and the
 RT locations of T7 generic elements.";
 RT J. Mol. Biol. 166:477-535(1983).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=82078034; PubMed=7310871;
 RX Dunn J.J.; Studier F.W.;
 RT "Nucleotide sequence from the genetic left end of bacteriophage T7
 DNA to the beginning of gene 4";
 RL J. Mol. Biol. 148:303-330(1981).
 CC !- FUNCTION: ENDODEOXYRIBONUCLEASE I, WHICH IS EXPRESSED IN THE LATE
 CC STAGE, IS NECESSARY FOR T7 GENETIC RECOMBINATION AND THE BREAKDOWN
 CC OF HOST DNA. IN THE EARLY STAGE OF INFECTION, T7 DNA REPLICATES AS
 CC A LINEAR MONOMER. IN THE LATE STAGE, THE T7 DNA REPLICATES VIA
 CC LINEAR CONCATENERS SEVERAL GENOMES IN LENGTH. THE GENE 3 PRODUCT
 CC HAS ALSO BEEN IMPLICATED IN THE MATURATION OF THESE CONCATENERS.
 CC !- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
 CC phospholigonucleotide end-products.
 CC
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 CC
 DR EMBL; V01127; CAA24345.1; -.
 DR PIR; B94615; NBBP37.
 DR PDB; 1FZR; 10-OCT-01.
 DR PDB; 1MOD; 10-JUL-02.
 DR PDB; 1M01; 18-DEC-02.
 DR InterPro; IPR005029; Phage_endo_I.
 DR Pfam; PF05367; Phage_endo_I_1.
 DR Hydrolase; Nuclease; Endonuclease; 3D-structure.
 SQ SEQUENCE 149 AA; 17172 MW; D092AA2BEE743BC1 CRC64;
 SQ
 Query Match 43.9%; Score 36; DB 1; Length 149;
 Best Local Similarity 58.3%; Pred. No. 31;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 AWTYASRGTRPGV 13
 Db 2 AGYGAKGTRKVG 13
 DE Metalloproteinase inhibitor 2 (TIMP-2) (Tissue
 DE metalloproteinases-2).
 GN TIMP2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TAXID=9986;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=9609920; PubMed=8548358;
 RX Wertheimer S.J.; Katz S.I.;
 RA "Molecular Cloning and Characterization of rabbit TIMP-2.";
 RT Inflamm. Res. 44:S121-S122(1995).
 OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OC Butheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Murinidae; Cricetinae;

[2]
 RN SEQUENCE OF 17-154 FROM N.A.
 RP STRAIN=New Zealand white;
 RC STRAIN=New Zealand white;
 RX MEDLINE=99057575; PubMed=9337780;
 RA Reno C.; Boykiw R.; Martinez M.L.; Hart D.A.;
 RT "Temporal alterations in mRNA levels for proteinases and inhibitors
 and their potential regulators in the healing media collateral
 ligament.";
 RT Biochem. Biophys. Res. Commun. 252:757-763(1998).
 RL FUNCTION: Complexes with metalloproteinases (such as collagenases)
 CC and irreversibly inactivates them.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- TIMP: The activity of TIMP is dependent on the presence of
 CC disulfide bonds (By similarity).
 CC !- SIMILARITY: Belongs to the TIMP family.
 CC !- SIMILARITY: Contains 1 NTR domain.
 CC
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 CC
 DR EMBL; AF069713; AAC95005.1; -.
 DR HSSP; P16035; 1BR9.
 DR InterPro; IPR001820; TIMP.
 DR InterPro; IPR00893; TIMP_like.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; NTR; 1.
 DR PROSITE; PS50189; NTR; 1.
 DR PROSITE; PS00288; TIMP; 1.
 DR Metalloprotease inhibitor.
 KW NTR.
 FT DOMAIN 1 126
 FT DISULFID 1 72
 FT DISULFID 3 101
 FT DISULFID 13 126
 FT DISULFID 128 175
 FT DISULFID 138 138
 FT DISULFID 146 167
 FT DISULFID 17 17
 FT CONFLICT 25 26
 FT CONFLICT 58 58
 FT CONFLICT 78 78
 FT CONFLICT 93 95
 FT CONFLICT 109 109
 FT CONFLICT 112 112
 FT CONFLICT 131 131
 SEQENCE 194 AA; 21849 MW; CDC8101A2D38C4A9 CRC64;
 Query Match 43.9%; Score 36; DB 1; Length 194;
 Best Local Similarity 63.6%; Prd. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

RESULT 39
 TIM2_RABBIT
 ID TIM2_RABBIT STANDARD; PRT; 194 AA.
 AC Q9TRZ7; O97589;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2004 (Rel. 43, Last sequence update)
 DE Metalloproteinase inhibitor 2 (TIMP-2) (Tissue
 DE metalloproteinases-2).
 GN TIMP2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TAXID=9986;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=9609920; PubMed=8548358;
 RX Wertheimer S.J.; Katz S.I.;
 RA "Molecular Cloning and Characterization of rabbit TIMP-2.";
 RT Inflamm. Res. 44:S121-S122(1995).
 OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OC Butheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Murinidae; Cricetinae;

RESULT 40
 TIM2_CRIIO
 ID TIM2_CRIIO STANDARD; PRT; 196 AA.
 AC Q60553;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Metalloprotease inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
 DE metalloproteinases-2) (Fragment).
 GN TIMP2.
 OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OC Butheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Murinidae; Cricetinae;

OC Cricetulus.
 OC NCBI_TaxID=10030;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA SUZUKI Y.;
 RI Submitted (NOV 1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
 CC and irreversibly inactivates them (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: The activity of TIMP2 is dependent on the presence of
 CC disulfide bonds (By similarity).
 CC -!- SIMILARITY: Belongs to the TIMP family.
 CC -!- SIMILARITY: Contains 1 NTR domain.

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DR EMBL; X75924; CAA5528.1; -.
 DR PIR; S38624; S38624.
 DR HSSP; P16235; 1B99.
 DR InterPro; IPR001220; TIMP.
 DR InterPro; IPR008993; TIMP_like.
 DR Pfam; PF00965; TIMP_1ike.
 DR SMART; SM00206; NTR; 1.
 DR PROSITE; PS50189; NTR; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KW Metalloprotease inhibitor; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 2
 FT CHAIN 3 196 BY SIMILARITY.
 FT DOMAIN 3 128 METALLOPROTEINASE INHIBITOR 2.
 FT DOMAIN 3 128 NTR.
 FT DISULFID 3 74 BY SIMILARITY.
 FT DISULFID 5 103 BY SIMILARITY.
 FT DISULFID 15 128 BY SIMILARITY.
 FT DISULFID 130 177 BY SIMILARITY.
 FT DISULFID 135 140 BY SIMILARITY.
 FT DISULFID 148 169 BY SIMILARITY.
 SQ SEQUENCE 196 AA; 21941 MW; 2DAB954AF75381 CRC64;

Query Match 43.9%; Score 36; DB 1; Length 196;
 Best Local Similarity 63.6%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
 Qy 1 CAWYASRGNDP 11
 Db 177 CAWY--RGAAP 185

Search completed: February 25, 2004, 06:42:59
 Job time : 13 secs

DE	C-RF amide.
OS	<i>Carausius auratus</i> (Goldfish).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; <i>Carausius</i> .
NCBI_TaxID	7957; [1] -
RN	SEQUENCE FROM N.A.
RC	TISSUE=brain;
RA	Satake H., Minakata H., Fujimoto M.;
RA	"Carausius" Ramide (C-RF amide)." ;
RA	Submitted (Nov-1998) to the EMBL/GenBank/DBJ databases.
EMBL	AB020024; BRA76652.1; -
DR	SEQUENCE 117 AA; 12879 MW; D5DC4FB22038C2B0 CRC64;
SG	Query Match 70.7%; Score 58; DB 13; Length 117; Best Local Similarity 66.7%; Pred. No. 0.026; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0; Qy 3 WYASRGIRPVGR 14 Db 63 WYVERGGVRDPIGR 74
RESULT 3	Q931Z7_991Z7 PRELIMINARY; PRT; 420 AA.
ID	991Z7_991Z7; AC
DT	01-DEC-2001 (TREMBrel. 19, Created)
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)
DE	Chain length factor-like protein.
AUR2B	OS Streptomyces aureofaciens.
Bacter	Actinobacteria; Actinomycetidae; Actinomycetales; Streptomyces; Streptomyces; Streptomyctaceae; Streptomyces.
NCBI_TaxID	1894; [1] -
RN	SEQUENCE FROM N.A.
RC	STRAIN=CCM3239; Kormanev J., Bistrikova J., Novakova R., Homerova D., Rezuchova B. ;
RT	"Cloning and characterization of a new polyketide gene cluster in Streptomyces aureofaciens CCM3239." ; Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
EMBL	AY033994; P29435; 1B3N.
DR	HSSP; GO:0003984; P: catalytic activity; IEA.
DR	GO:0006633; P:fatty acid biosynthesis; IEA.
DR	InterPro: IPR000794; Ketoacyl-synthetase.
DR	Pfam; PF00103; ketoacyl-synthetase.
DR	Pfam; PF02801; ketoacyl-synthetase.
DR	SEQUENCE 420 AA; 43011 MW; 3C2722BE88C2DEA CRC64;
SG	Query Match 55.5%; Score 45.5; DB 2; Length 420; Best Local Similarity 55.6%; Pred. No. 16; Matches 10; Conservative 2; Mismatches 1; Indels 5; Gaps 1; Qy 2 AWYAS-----RGIRPVGR 14 Db 37 AWWAVLRLGESEGRPVGR 54
RESULT 4	Q8VYUB9_08VYUB9 PRELIMINARY; PRT; 515 AA.
ID	08VYUB9_08VYUB9; AC
DT	01-MAR-2002 (TREMBrel. 20, Created)
DT	01-MAR-2002 (TREMBrel. 20, Last sequence update)
DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)
DE	Chlorin reductase subunit Y.
GN	Bacter
OC	<i>Bradyrhizobium</i> sp. ORS278.
OC	Bacteria; Proteobacteria; Alpha proteobacteria; Rhizobiales;
NCBI_TaxID	14615; [1] -
RN	SEQUENCE FROM N.A.
RC	STRAIN=ORS278; MEDLINE=00570559; PubMed=11114184; "Effect of <i>Bradyrhizobium</i> photosynthesis on stem nodulation of <i>Aschynomene sensitiva</i> ,"
RA	Giraud E., Hannibal L., Fardoux J., Vermeglio A., Dreyfus B. ;
RT	Proc. Natl. Acad. Sci. U.S.A. 97:14795-14800 (2000).
DR	AF182374; AA168657.1; -
SQ	SEQUENCE 515 AA; 54.96 MW; 9170EB108FA547F CRC64;
Query Match 54.9%; Score 45; DB 2; Length 515; Best Local Similarity 70.0%; Pred. No. 24; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Qy 1 CAWWSRGIR 10 Db 382 CAWWSRGIVR 391	
RESULT 5	Q8P3J9_08P3J9 PRELIMINARY; PRT; 141 AA.
ID	08P3J9; AC
DT	01-OCT-2002 (TREMBrel. 22, Created)
DT	01-OCT-2002 (TREMBrel. 22, Last sequence update)
DT	01-JUN-2003 (TREMBrel. 24, Last annotation update)
DE	Protein-export membrane protein.
GN	SECG or XAC276.
OS	Xanthomonas axonopodis (pv. citri).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
NCBI_TaxID	98289; [1] -
RN	SEQUENCE FROM N.A.
RC	STRAIN=3016 / ATCC 13902 / XV 101; MEDLINE=3202145; PubMed=12024237;
RA	da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitello C.B., Van Silvius M.A., Almeida N.P., Alves L.M.C., do Amaral A.M., Bertoloni C.M.C., Camargo F., Ciapina J., Camarotti G., Cannavan F., Cardozo J., Chamberg F., Ciapina J., Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira J., Gomes J.S., Ferreira-Santos J.R., Ferro M.I.T., Formighieri E.F., Franco M.C., Greiggi C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.E., Locardi B.C., Machado M.A., Madeira M.A.B.N., Martinez-Rossi N.M., Martins E.C., Medanis J., Menck C.F.M., Miyataki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Senna J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White P.F., Serubbi J.C., Kitajima J.P., "Comparison of the genomes of two <i>Xanthomonas</i> pathogens with differing host specificities,"
RT	Nature 417:455-463 (2002).
DR	EMBL; AB011910; AA037551.1; -
DR	GO: GO:0016021; C: integral to membrane; IEA.
DR	GO: GO:0015450; P: protein translocase activity; IEA.
DR	InterPro: IPR004652; SecG.
DR	Pfam; PF03840; SecG; 1.
DR	PRINTS; PRO1611; SECGBREPORT.
KW	Complete Proteome.
SQ	SEQUENCE 141-AA; 13864 MW; CC8009663B05F5CA CRC64;
Query Match 53.7%; Score 44; DB 16; Length 141; Best Local Similarity 70.0%; Pred. No. 8.8; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Qy 2 AWYASRGTRP 11	

56 AWYATHGARP 65

Db	RESULT 6	Q8P771 PRELIMINARY; PRT; 146 AA.	RX MEDLINE=22709107; PubMed=12788972;
	AC Q8P771;		RA Garnier T., Biglmaier K., Camus J.-C., Medina N., Mansoor H., Monsepe C., Monsepe C., Simon S., Wheeler P.R.,
	DT 01-OCT-2002 (TREMBLrel. 22, Created)		RA Duthoy S., Grondin S., Lacroix C., Keating L., Mayes R.,
	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)		RA Atkin R., Barrell B.G., Cole S.T., Gordon S.V., Hewlinson R.G., Parhill J.,
	DE protein-export membrane protein.		RA "The complete genome sequence of <i>Mycobacterium bovis</i> ," RT RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
GN	SGC OR XC22530.		DR EMBL; BX48335; CAD93299.1; -.
OS	Xanthomonas campestris (pv. campestris).		KW Complete proteome.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.		SQ 302 AA; 32592 MW; 2A0EF63A3B50D77 CRC64;
OX	NCBI_TaxID=340;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 33913 / NCPPB 528;		
RX	MEDLINE=22022145; PubMed=12024217;		
RA	Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,		
RA	Alves L.M.C., do Amaral A.M., Berilo J., Camargo L.E.A.,	PRT; 315 AA.	
RA	Camargo G., Cannavaro P., Cardozo J., Chamborg P., Ciapina L.P., Cicarelli R.M.B., Coutinho L.D., Cursino-Santos J.R., Bi-Dorzy H.,	ID P96274 PRELIMINARY; PRT; 315 AA.	
RA	Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.P., Franco M.C., Greggio C.C., Gruber A., Katsiyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Martins E.C., Meidanis J., Madeira A.M., Machado M.A.,	ID P96274 PRELIMINARY; PRT; 315 AA.	
RA	Martins L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.P., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Xitajima J.P.,	ID P96274 PRELIMINARY; PRT; 315 AA.	
RT	"Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."		
RT	RL MEDLINE=417459-663 (2002).		
DR	EMBL; AE012364; AAM1802.1; -.		
DR	GO:0016021; C: integral to membrane; IEA.		
DR	GO:0015450; P: protein translocation; IEA.		
DR	GO:0009306; P: protein secretion; IEA.		
DR	InterPro:IPR004692; SecG.		
DR	PRINTS:PRO1651; SECEXPORT.		
DR	Complete proteome; PRO1651; SECEXPORT.		
KW	SEQUENCE 146 AA; 14481 MW; 503AABAD982C04CB CRC64;		
SQ			
Query Match	Best Local Similarity 70.0%; Matches 7; Conservative 7; Mismatches 1; Pred. No. 9.1; Indels 0; Gaps 0;		
Qy	2 AWYASRGIRP 11		
Db	56 AWYATHGARP 65		
RESULT 7	Q7U207 PRELIMINARY; PRT; 302 AA.		
ID	Q7U207 PRELIMINARY; PRT; 302 AA.		
AC	Q7U207; DT 01-OCT-2003 (TREMBLrel. 25, Created)		
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.		
GN	MB0436C.		
OS	Mycobacterium bovis.		
OC	Bacteria; Actinobacteria; Actinomycetales; Actinomycetales; Corynebacterineae; Mycobacterium.		
OC	NCBI_TaxID=1765;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=AF2122/97;		
RX	MEDLINE=98295987; PubMed=9534230;		
RA	Colle S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cole S.T., Eiglmeier K., Barry C.E. III, Tekala F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R.J., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Horstby T., Jages K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Snelton S., Squares S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Weidman J., Khouli H., Gill J., Mikula A., Delcher A., Utterback T., Weidman J., Khouli H., Gill J., Mikula A., Bisbasi W.,		
RT	"Whole genome comparison of <i>Mycobacterium tuberculosis</i> clinical and laboratory strains."		
RT	RL Submitted (AFR-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; CAB06568.1; ALT_INIT.		
DR	EMBL; AB006947; AAK44666.1; -.		
DR	PTR; B70631; B70631.		
DR	TIGB; MT0443; -.		
DR	Tuberculist; Rv0428C; -.		
KW	Hypothetical protein; Complete proteome.		
SQ	SEQUENCE 315 AA; 34099 MW; 3BEE6399C4C0C7B7 CRC64;		
Query Match	Best Local Similarity 70.0%; Matches 7; Conservative 7; Mismatches 1; Pred. No. 21; Indels 0; Gaps 0;		
Qy	2 AWYASRGIRP 11		
Db	56 AWYATHGARP 65		

Db	139 AWYASRDLOP 148	Qy	2 AWYASRGIRP 11
		Db	79 SWLASRGIKP 88
RESULT 9			
Q8ZTH7	PRELIMINARY;	PRT;	273 AA.
AC	Q8ZTH7;		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Morphine 6-dihydrogenase, conjectural.		
GN	PAE247.		
OS	Pyrococcus aerophilum.		
OC	Archaea; Crenarchaeota; Thermoproteales;		
OC	Thermoproteaceae; Pyrococcus.		
OX	NCBI_TaxID=13773;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=JM2 / ATCC 51768 / DSM 7523;		
RX	MEDLINE=1664397; PubMed=11792860;		
RA	Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I., Miller J.H. "Genome sequence of the hyperthermophilic crenarchaeon Pyrococcus aerophilum." Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).		
RT			
RL	EMBL; AE009920; AL64784.1; -.		
DR	InterPro; IPR01335; Aldo/ket_red.		
DR	PFam; PF00248; aldo_ket_red_1.		
DR	PRINTS; PR00069; ALDKEFDTAE.		
DR	ProDom; PD00388; Aldo/ket_red_1.		
KW	Complete proteome.		
SQ	SEQUENCE 273 AA; 30203 MW; 3F9D1208FB10DF7F CRC64;		
Query Match	52.4%; Score 43; DB 17; Length 273; Best Local Similarity 54.5%; Pred. No. 27; Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
Qy	2 AWYASRGIRP 12		
Db	228 AWYVVRGVVFI 238		
RESULT 10			
Q9F642	PRELIMINARY;	PRT;	326 AA.
AC	Q9F642;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
MXCA			
GN	Stigmatella aurantiaca.		
OS	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterinae; Cystobacteraceae; Stigmatellia.		
OC			
NCBI_TaxID=41;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SG_a15;		
DR	Medline=0495524; PubMed=11029592;		
RA	Silakowski B., Kunze B., Nordsiek G., Blocker H., Hofle G., Muller R.; "The myxocellin iron transport region of the myxobacterium Stigmatella aurantiaca. Bur. J. Biochem. 267:6476-6685 (2000)."		
RL	EMBL; AF299336; AA331124.1; -.		
DR	InterPro; IPR001395; Aldo/ket_red.		
DR	PFam; PF00248; aldo_ket_red_1.		
DR	ProDom; PD00388; Aldo_ket_red_1.		
SQ	SEQUENCE 326 AA; 35086 MW; 5C7979492B161DFF CRC64;		
Query Match	52.4%; Score 43; DB 2; Length 326; Best Local Similarity 70.0%; Pred. No. 32; Matches 2; Mismatches 1; Indels 0; Gaps 0;		
Qy	2 AWYASRGIRP 13		
Db	85 AWFAEDGLKEAG 96		
RESULT 11			
Q8816	PRELIMINARY;	PRT;	402 AA.
AC	Q8816;		
DT	01-JUN-2003 (TREMBLrel. 24, Created)		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DB	Putative exoribonuclease large subunit.		
GN	XSEA OR SAV3211.		
OS	Streptomyces avermitilis.		
OC	Bacteria; Actinobacteria; Actinomycetaceae; Streptomyces.		
OX	NCBI_TaxID=33903;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRRL 8165;		
RX	MEDLINE=21477403; PubMed=11572948;		
RA	Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osono T., Kikuchi H., Shiba T., Sekine K., Hattori M.		
RA	"Genomic sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites";		
RT	Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).		
RL	[2]		
RN	SEQUENCE FROM N.A.		

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandt R.C., Rogers Y.-H.-G., Blazquez R.G., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.B., Abrial J.F., Agbayani A., An H.-J., Andrew-Pfannkoch C., Baldwin D., Ballew M.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Botchkova D., Bouck M.R., Bouck J., Brockstein P., Brottier P., Burtis K.C., Busam D.A., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabreiel A.E., Garg N.S., Gelb B.W., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin T., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kralovicz S., Kulp D., Lai Z., Lasko P., Lei Y., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount M., Moy M., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shew H., Shue B.C., Siden-Klamos I., Simpson M., Stupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector E., Turner E., Venter J., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang Q.A., Ye J., Yeh R.-P., Zaveri J.S., Zhang M., Zhang Q., Zhao Q., Zheng L., Zheng X.-H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT "The genome sequence of *Drosophila melanogaster*," Science 287:2185-2195 (2000). RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. RN [2]

RP SEQUENCE FROM N.A. RA Celniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C., Gocayne J.D., Sinden K., Simpson M., Stupski M.P., Smith T., Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Chamb M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dransfield D., Ferreira S., Frise E., Gallo R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson J., Patel S., Pacleb J., Paragas V., Park S., Pfeiffer B., Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svartkar S., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; RT "Sequencing of *Drosophila melanogaster* genome," RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. RN [3]

RP SEQUENCE FROM N.A. RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celikker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutriak F., Whitfield E., Ashburner M., Gellibert W.M., Rubin G.M., Mungall C.J., Lewis S.E.; RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. RN [4]

RP SEQUENCE FROM N.A. RA Adams M.D., Celikker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. RN [5]

RP SEQUENCE FROM N.A. RA Flybase; FBgn0051619; CG31619. RA DR Flybase; FBgn0051619; CG31619. DR InterPro; IPR003599; Ig, Ig-like. DR InterPro; IPR007110; Ig, Ig-like. DR InterPro; IPR003598; Ig, Ig-like. DR InterPro; IPR00884; TSP1. DR Pfam; PF00047; ig; Ig. DR Pfam; PF00090; tsp_1; Ig. DR SMART; SN00403; Ig; Ig. DR SMART; SN00408; IgG2; Ig. DR SMART; SN00209; TSP1; Ig. DR SMART; PS50835; IgG Ig-like; Ig. DR PROSITE; PS50092; TSP1; Ig. DR ImmunoGlobulin domain. KW SEQUENCE 1393 AA; 150210 MW; F83CDB090964272F CRC64; SQ Query Match 52.4%; Score 43; DB 5; Length 1353; Best Local Similarity 61.5%; Pred. No. 1.5e+02; Matches 8; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 CAVWYASGRIPVG 13 Db 1.272 CWWTGSRR--RPAG 1282

RESULT 16 Q8UG50 PRELIMINARY; PRT; 105 AA. ID Q8UG50 PRELIMINARY; PRT; 105 AA. AC DT 01-JUN-2002 (TREMBLrel. 21, Created) DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update) DT 01-JUN-2003 (TREMBLrel. 21, Last annotation update) DE Hypothetical protein Atul191. ATU1191 OR AGR_C_2196. GN Agrobacterium tumefaciens (strain C58 / ATCC 33970). OS Agrobacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales; OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhizobium group; Agrobacterium; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium. NCBI-TaxID=176299; RN [1] SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RX MEDLINE=21608551; PubMed=11743193; RX MEDLINE=21608550; PubMed=11743194; RX MEDLINE=21608550; PubMed=11743194; RA Wood D.W., Setubal J.C., Kaul R., Monks D.B., Kitajima J.J.P., Okura V.K., Zhou Y., Chen L., Wood G.B., Almeida N.F. Jr., Woo L., RA Chen Y., Puulsen I.T., Biesen J.A., Karp P.D., Bovee D. Sr., RA Chapman P., Clandenning J., Deatherage G., Gillett W., Grant C., RA Kuyaviv T., Levy R., Li M.-J., Clelland E., Palmieri A., Gordon D., RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., RA Nester B.W.; RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58," RT Science 294:2317-2323 (2001). RN [2]

RP SEQUENCE FROM N.A. RX MEDLINE=21608551; PubMed=11743194; RA Goodier B., Hinkle G., Gattung S., Miller N., Blanchard M., Quroilo B., Goldman B.S., Cao Y., Askenazi M., Hailing C., Mullin L., RA Houlden K., Gordon J., Vaudin M., Marichou O., Epp A., Liu F., RA Wollman C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., RA Flangan C., Crowell C., Lomo C., Sear C., Strub G., Cielo C., Slater S.; RT "Genomic sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58," RT Science 294:2317-2323 (2001). RN [3]

RP SEQUENCE FROM N.A. RX MEDLINE=21608551; PubMed=11743194; RA Goodier B., Hinkle G., Gattung S., Miller N., Blanchard M., Quroilo B., Goldman B.S., Cao Y., Askenazi M., Hailing C., Mullin L., RA Houlden K., Gordon J., Vaudin M., Marichou O., Epp A., Liu F., RA Wollman C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., RA Flangan C., Crowell C., Lomo C., Sear C., Strub G., Cielo C., Slater S.; RT "Genomic sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58," RT Science 294:2317-2323 (2001). RN [4]

RP SEQUENCE FROM N.A. RA Flybase; FBgn0051619; CG31619. DR Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases. RN [5]

RP SEQUENCE FROM N.A. RA Flybase; FBgn0051619; CG31619. DR Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases. RN [6]

RP SEQUENCE 105 AA; 11749 MW; 0053AAE20849A1D0 CRC64; SQ Query Match 51.2%; Score 42; DB 16; Length 105;

Best Local Similarity 66.7%; Pred. No. 14; Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRCIR 10
Db 54 AWYAAARGVQ 62

RESULT 17

Q8YL78 PRELIMINARY; PRT; 113 AA.

AC Q8YL78; PubMed=11759840; CREATED; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein Airf057.

GN ALR7057.

OS Anabaena sp. (strain PCC 7120).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI_TaxID=103630;

RN SEQUENCE FROM N.A.
RX MEDLINE# 200205285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsunoto M., Matsuno A., Muraki A., Nakazawa M., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
RA "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213 (2001).
DR PIR; AL2484; AL2484.
DR GO; GO:0046800; DBP03600; DRB78141.1.; -.
DR GO; GO:0046821; DBA2484.
DR Plasmid; Hypothetical Protein; Complete proteome.
SQ SEQUENCE 113 AA; 13058 MW; CF5ED411086C0A3 CRC64;

Query Match 51.2%; Score 42; DB 16; Length 113;

Best Local Similarity 70.0%; Pred. No. 15; Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AWYASRGIRP 11
Db 64 AWYAKAGIEP 73

RESULT 18

Q9PGJ6 PRELIMINARY; PRT; 132 AA.

AC Q9PGJ6; PubMed=10910347; CREATED; DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Protein-export membrane protein.

OS Xylella fastidiosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xylella.

RC STRAIN 9a5c; MEDLINE# 20335717; PubMed=10910347;
RX Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Aencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Bapista C.S., Barros M.H., Bonacorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa Neto C.M., Coutinho L.L., Cristofani M., Dias Neto E., Docena C., El-Dorry H., Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furian L.R., Gruber A., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.A., Nascimento A.J.T.O., Netto L.B.S., Nhami A., Jr., Oliveira F.G., Nunes L.R., Oliveira M.A., Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A., Peixoto B.R., Pereira G.A., Pereira H.A., Jr., Pequero J.B., Quaggio R.B., Roberto P.G., Rodriguez V., de Rosa A.J.M., de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva P.B., Silva W.A., Jr., da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsunako M.H., Valiada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zagó M.A., Zatz M., Meidanis J., Setubal J.C., "The genome sequence of the plant pathogen *Xylella fastidiosa*."; DR EMBL; AB003893; AAF83115.1.; -.

DR PIR; BB2824; BB2824.

DR GO; GO:0016021; Cintegral to membrane; IEA.
DR GO; GO:0015450; F:protein translocase activity; IEA.
DR GO; GO:0009306; F:protein secretion; IEA.

DR InterPro; IPR004632; SecG.
DR Pfam; PF0840; SecG; 1.

DR PRINTS; PRO151; SECGBEXPORT.
DR TIGRFAMS; TIGR00810; SECGB.
DR Complete proteome; TIGR00810; SECGB.
KW SEQUENCE 132 AA; 13530 MW; 757240DD2D7A1308 CRC64;

Query Match 51.2%; Score 42; DB 16; Length 132;
Best Local Similarity 61.5%; Pred. No. 18; Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVG 14
Db 70 AWYASRGHAVAQ 82

RESULT 19

Q87EQ6 PRELIMINARY; PRT; 132 AA.

AC Q87EQ6; CREATED; DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Protein-export membrane protein SECg.
GN SECg OR PD0246.

OS Xylella fastidiosa (strain Temecula / ATCC 700964).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xylella.

OC Xanthomonadales; Xylella.

RN [1] NCBI_TaxID=18190;

RN SEQUENCE FROM N.A.

RX MEDLINE# 2242331; PubMed=12533478;

RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Miyaki C.Y., Furian L.R., Camargo L.E.A., da Silva A.C.R., Goldman M.H.S., Goldman G.H., Ferro M.I.T., da Silva P.R., Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimura E.T., Ferro E.S., Harrakava R., Kuramae E.B., Marino C.L., Giglioti B., Abreu I.L., Alves L.M.C., do Amaral A.M., Baia G.S., Bianco S.R., Brito M.S., Cannavan F.S., Celestino A.V., da Cunha A.P., Ferreira R.C., Ferro J.A., Formighieri E.F., Kishii L.T., Leoni S.G., Oliveira A.R., Rosa V.E., Jr., Sasaki F.T., Sena J.A.D., de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G., Civerola E.L., Simpson A.J.G., Almeida N.F., Setubal J.C., Kitajima J.P., "Comparative analyses of the complete genome sequences of Pierce's RT disease and citrus variegated chlorosis strains of *Xylella* RT fastidiosa."; RT J. Bacteriol. 185:1018-1026 (2003).

DR EMBL:AE012554; AAQ28133.1; - .
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0015450; F: protein translocase activity; IEA.
 DR GO: GO:0009306; P: protein secretion; IEA.
 DR InterPro:IPR004592; SecC.
 PFam: PF0840; SecG; 1.
 PRINTS: PRO1651; SECGEEXPORT.
 KW Complete proteome; IEA.
 SEQUENCE 132 AA; 13605 MW; 67604062CC77808 CRC64;
 Query Match 51.2%; Score 42; DB 16; Length 132;
 Best Local Similarity 61.5%; Pred. No. 18;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 AWYASRGIRGVGR 14
 Db 70 AWYASRGHISVAQ 82
 RESULT 20
 Q8RTA3 Q8RTA3 PRELIMINARY; PRT; 223 AA.
 ID Q8RTA3; PRELIMINARY; PRT; 223 AA.
 AC DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE LICD2 (Fragment).
 OS Streptococcus pneumoniae.
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.
 OC NCBI_TaxID=11313;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=NFA44.1.
 RC Weier J.N., Bae D.H.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AF067751; AAI77432.1; - .
 DR InterPro:IPR007074; LicD.
 PFam: PF04991; LicD; 1.
 FT NON_TER 223 223
 SEQUENCE 223 AA; 26566 MW; COFC93A7AC75384 CRC64;
 Query Match 51.2%; Score 42; DB 2; Length 223;
 Best Local Similarity 54.5%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 CAYWASRGIRP 11
 Db 166 CSWYALRFVNP 176
 RESULT 21
 Q912F2 Q912F2 PRELIMINARY; PRT; 250 AA.
 ID Q912F2; PRELIMINARY; PRT; 250 AA.
 AC DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DR Hypothetical protein PA1952.
 GN PA1952.
 OS Pseudomonas aeruginosa.
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 OC NCBI_TaxID=287;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=ATCC 15692 / PAO1;
 RC MEDLINE=2043237; PubMed=10984043;
 RX Stover C.K., Pham X.-Q.T., Orwin A.L., Miooguchi S.D., Warrener P.,
 Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 opportunistic pathogen";
 RL Nature 406:959-964 (2000).
 DR EMBL: AE004622; AA05340.1; - .
 DR PIR; G83400; GS3400.
 DR InterPro: IPR00437; PROKAR_LIPOPROBTIN; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROBTIN; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 250 AA; 25619 MW; B997F6BE28D792C2 CRC64;
 Query Match 51.2%; Score 42; DB 16; Length 250;
 Best Local Similarity 53.8%; Pred. No. 36;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CAYWASRGIRGVGR 13
 Db 237 CAYWASRGIRGVGR 249
 RESULT 22
 Q8CWRI Q8CWRI PRELIMINARY; PRT; 269 AA.
 ID Q8CWRI; PRELIMINARY; PRT; 269 AA.
 AC DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DR 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE LicD Protein.
 GN LICD2 OR SPR152.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.
 OC NCBI_TaxID=1710101;
 RN [1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.; PubMed=11544234;
 RX MEDLINE=21429245;
 RA Hoskins J., Alborn W.E., Jr., Arnold J., Blaszczaik L.C., Burgett S.,
 Dehoff B.S., Estrem S.T., Fritz J., Fu D.J., Fuller W., Geringer C.,
 Gilmour R., Glass J.S., Khoja H., Kratt A.R., Lagace R.E.,
 LeBlanc D.J., Lee L.N., Lefcowitz B.J., Lu J., Mundy C.W.,
 McAhern S.M., McHenney M., McLeaster K., Niccas T.I.,
 Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
 Sun P.-M., Winkler M.E., Yang Y., Young D., Zhao G.,
 Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
 Glass J.I.;
 RA Genome of the bacterium *Streptococcus pneumoniae* strain R6.;"
 DR J. Bacteriol. 183:709-5717 (2001).
 DR PIR; A95148; A95148.
 DR PIR; A95148; A95148.
 DR PIR; G98015; G98015.
 DR PFam: PF04991; LicD; 1.
 DR InterPro: IPR007074; LicD.
 KW Complete proteome.
 SQ SEQUENCE 269 AA; 32100 MW; 31A152DFAA480A10 CRC64;
 Query Match 51.2%; Score 42; DB 16; Length 269;
 Best Local Similarity 54.5%; Pred. No. 39;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 CAYWASRGIRP 11
 Db 166 CAYWASRGIRP 176
 RESULT 23
 Q9X4D5 Q9X4D5 PRELIMINARY; PRT; 269 AA.
 ID Q9X4D5; PRELIMINARY; PRT; 269 AA.
 AC Q9X4D5; PRELIMINARY; PRT; 269 AA.
 DR DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DR DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE LICD.
 GN LICD2 OR SP1274.

OS Streptococcus pneumoniae.	RX MEDLINE=22608306; PubMed=12692562;
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	RA Ikeda H.; Ishikawa J.; Hamamoto A.; Shinose M.; Kikuchi H.; Shiba T.,
OC Streptococcus.	RA Sakai Y.; Hattori M.; Omura S.;
OX NCBI_TaxID=1313;	RT "Complete genome sequence and comparative analysis of the industrial
RN [1]	RT microorganism Streptococyes avermitilis."
RP SEQUENCE FROM N.A.	RT
RC STRAIN=R6X;	RL Nat.; Biotechnol. 21:526-531 (2003).
RX MEDLINE=99117023; PubMed=10200966;	DR EMBL: AP005038; BAC71990.1;
RA Zhang J.R.; Idanpaan-Heikkila I.; Fischer W.; Tuomanen E.I.;	DR GO: GO:0008080; P:N-acetyltransferase activity; IBA.
RT "Pneumococcal LicD2 gene is involved in phosphorylcholine	DR InterPro; IPR000182; NCASafety_trans.
RT metabolism.";	DR Pfam; PF00533; Acetyltransf.
RT Mol. Microbiol. 31:1477-1488 (1999).	KW Hypothetical protein; Complete protein.
RN [2]	SQ SEQUENCE 288 AA; 31063 MW; 2775CR154741DB3 CRC64;
RP SEQUENCE FROM N.A.	Query Match 51.2%; Score 42; DB 16; Length 288;
RC STRAIN=ATCC BAA-334 / TIGR4; PubMed=11463916;	Best Local Similarity 58.3%; Pred. No. 42;
RX MEDLINE=21357209; PubMed=21357209;	Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
RA Tettelin H.; Nelson K.E.; Paulsen I.T.; Eisen J.A.; Read T.D.,	AC 2 AWYASRGIRPVG 13
RA Heidelberg J.; DeBoy R.T.; Haft D.H.; Dodson R.J.,	DB 249 AWLKERGLAPVG 260
RA Durkin A.S.; Gwin M.; Kolonay J.F.; Nelson W.C.; Peterson J.D.,	RESULT 25
RA Umayam L.A.; White O.; Salzberg S.L.; Lewis M.R.; Radune D.,	Q83N5 PRELIMINARY; PRT; 289 AA.
RA Holtzapfel B.; Khorri H.; Wolf A.M.; Utterback T.R.; Fansen C.L.,	ID Q83N5 PRELIMINARY; PRT; 289 AA.
RA McDonald L.A.; Feldblyum T.V.; Anguilo S.; Dickinson T.; Hickey E.K.,	AC Q83N5 PRELIMINARY; PRT; 289 AA.
RA Holt I.E.; Loftus B.J.; Yang F.; Smith H.O.; Venter J.C.,	DT 01-JUN-2003 (TREMBLrel. 24; Created)
RA Dougherty B.A.; Hollingshead S.K.; Fraser C.M.,	DT 01-JUN-2003 (TREMBLrel. 24; Last sequence update)
RT "Complete genome sequence of a virulent isolate of Streptococcus	DE Bir3843 protein.
RT pneumoniae.";	GN BLR3843
RT EMBL; AF10539; AAD31094.1; -.	OS Bradyrhizobium japonicum.
RT DR	OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhizobiales;
RT PIR; A95148; A95148.	OC Bradyrhizobiaceae; Bradyrhizobium.
RT PIR; G98015; G98015.	OX NCBI_TaxID=375;
RT TIGR; SP1274; -.	RN [1]
RT InterPro; IPR007074; LicD.	RP Complete proteome; 9:189-197 (2002).
RT Pfam; PF04991; LicD; 1.	DR EMBL; AP005949; BAC49108.1; -.
RW Complete proteome.	KW Complete proteome; 32151 MW; 30D4B03A4ED8A3FD CRC64;
SQ SEQUENCE 269 AA; 32100 MW; 31A152DFAA480A10 CRC64;	RC SEQUENCE FROM N.A.
Query Match 51.2%; Score 42; DB 16; Length 269;	RC STRAIN=USDA 110; RX MEDLINE=2481998; PubMed=125997275;
Best Local Similarity 54.5%; Pred. No. 39;	RA Kaneko T.; Nakamura Y.; Sato S.; Minamisawa K.; Uchiumi T.,
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	RA Sasamoto S.; Watanabe K.; Tadesawa K.; Iriuchibhi M.; Kawashima K.,
QY 1 CAYWASRGIRPV 11	RA Kohara M.; Matsumoto M.; Shimpo S.; Tsuruoka H.; Wada T.; Yanada M.,
Db 166 CSWYALRFVNP 176	RA Tabata S.;
OS Streptomyces avermitilis.	RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;	RT Bradyrhizobium japonicum; USDA110.";
OC Streptomyces; Streptomyceae; Streptomyces.	RT DNA Res. 9:189-197 (2002).
OX NCBI_TaxID=33903;	DR EMBL; AP005949; BAC49108.1; -.
RN [1]	KW Complete proteome; 32151 MW; 30D4B03A4ED8A3FD CRC64;
RP SEQUENCE FROM N.A.	Query Match 51.2%; Score 42; DB 16; Length 288;
RC STRAIN=MA-6680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	Best Local Similarity 60.0%; Pred. No. 42;
RX MEDLINE=21477403; PubMed=11572948;	Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
RA Omura S.; Ikeda H.; Ishikawa J.; Hamamoto A.; Takahashi C.,	AC Q9LM51 PRELIMINARY; PRT; 487 AA.
RA Shinose M.; Takahashi Y.; Horikawa H.; Nakazawa H.; Osono T.,	AC Q9LM51 PRELIMINARY; PRT; 487 AA.
RA Kikuchi H.; Shiba T.; Sakai Y.; Hattori M.;	DT 01-OCT-2000 (TREMBLrel. 15; Created)
RT "Genome sequence of an industrial microorganism Streptomyces	DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)
RT avermitilites"; deducing the ability of producing secondary	DE F2E2.15.
RT metabolites";	OS Arabidopsis thaliana (Mouse-ear cress).
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).	OC Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
RN [2]	OC Eudicots; core eudicots; rosids;
RP SEQUENCE FROM N.A.	OC Eurosidis II; Brassicales; Brassicaceae; Arabidopsis.
RX STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	OX NCBI_TaxID=3722; RN [1]

RP SEQUENCE FROM N.A.
 Shim P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altaifi H., Bei Q., Chin C., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Toriumi M., Vaysberg M., Yu G., Federer J.R., Theologis A., Ecker J.R.; "Genomic sequence for *Arabidopsis thaliana* BAC F2E2 from chromosome 1." Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 RL [2]
 RN
 RP SEQUENCE FROM N.A.
 Ecker J.R.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 RL [3]
 RN
 RP SEQUENCE FROM N.A.
 Ecker J.R.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 Cheek R., Shim P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altaifi H., Bei B., Chin C., Choi E., Choi B., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Toriumi A., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RL [5]
 DR AC069254; ARAP86559.1; -
 SQ SEQUENCE 487 AA; 55018 MW; DC46E10FASAD679 CRC64;
 Query Match 51.2%; Score 42; DB 10; Length 487;
 Best Local Similarity 54.5%; Pred. No. 74; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 CAYWASRGIRPV 11
 Db 126 CAWTTLSNHVEP 136

RESULT 28
 DR PROSITE; PS50090; MYB 3; 1;
 KW DNA-binding; Nuclear Protein;
 SQ SEQUENCE 645 AA; 70455 MW; D184A30CCFB3EA77 CRC64;
 Query Match 51.2%; Score 42; DB 10; Length 645;
 Best Local Similarity 63.6%; Pred. No. 1e+02; Indels 2; Mismatches 7; Conservative 2; Nis matches 2; Indels 0; Gaps 0;
 RT
 Qy 2 AWYASRGIRPV 12
 Db 357 AWWASHGLLPPV 367

RESULT 29
 DR Q95N04; PRELIMINARY;
 ID Q95N04; PRELIMINARY;
 AC Q95N04; PRELIMINARY;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DR Dihydrorollipamide acetyltransferase precursor (EC 2.3.1.12).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9833;
 RN [1]
 DR SEQUENCE FROM N.A.
 RA Koike K.;
 RT "Isolation and characterization of the cDNA encoding the dihydrorollipamide acetyltransferase component of the porcine pyruvate dehydrogenase complex.";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIUM (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 LIPOYL-BINDING DOMAINS.
 DR EMBL_AB036739; BAB61722.0.1;
 DR GO; GO:0005739 C:mitochondrion; IEA.
 DR GO; GO:0045254 C:pyruvate dehydrogenase complex; IEA.
 DR GO; GO:0008415 F:acyltransferase activity; IEA.
 DR GO; GO:0005524 F:AMP binding; IEA.
 DR GO; GO:0004743 F:hydrolipamide S-acetyltransferase activity; IEA.
 DR GO; GO:0005515 F:protein binding; IEA.
 DR GO; GO:0016740 F:transferase activity; IEA.
 DR GO; GO:004812; F:RNA ligase activity; IEA.
 DR GO; GO:0006418 F:amino acid activation; IEA.
 DR GO; GO:0006956 F:glycolysis; IEA.
 DR InterPro; IPR001078; 2oxoacid_dh.
 DR InterPro; IPR06257; AceF long.
 DR InterPro; IPR00089; Biotin_lipoyl.
 DR InterPro; IPR04167; E3 binding.
 DR InterPro; IPR03016; Lipoyl_BS.
 DR InterPro; IPR01412; tRNA-synth_I.
 DR Pfam PF00198; 2-oxoacid_dh.
 DR Pfam PF00364; biotin_lipoyl; 2.
 DR Pfam PF02817; e3_binding; 1.
 DR Prodrom; PD001115; 2oxoacid_dh; 1.
 DR TIGRFAMs; TIGR01349; PDIC_trf_mito; 1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 DR PROSITE; PS00189; Lipoyl; 2.
 KW Acyltransferase; Lipoyl; Signal; Transferase; Mitochondrion.
 FT SIGNAL 1 86
 FT CHAIN 87 647
 SQ SEQUENCE 647 AA; 69014 MW; 3BB554B0D5F8235E CRC64;
 Query Match 51.2%; Score 42; DB 6; Length 647;
 Best Local Similarity 50.0%; Pred. No. 1e+02; Indels 6; Mismatches 1; Nis matches 1; Gaps 0;

RESULT 27
 DR Q81713 PRELIMINARY;
 ID Q81713; PRELIMINARY;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Late elongated hypocotyl protein.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Viridiplantae; Streptophytina; Tracheophyta.
 OC Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]

RESULT 28
 DR PROSITE; PS50090; MYB 3; 1;
 KW DNA-binding; Nuclear Protein;
 SQ SEQUENCE 645 AA; 70455 MW; D184A30CCFB3EA77 CRC64;
 Query Match 51.2%; Score 42; DB 6; Length 645;
 Best Local Similarity 50.0%; Pred. No. 1e+02; Indels 6; Mismatches 1; Nis matches 1; Gaps 0;

RESULT 29
 DR Q95N04; PRELIMINARY;
 ID Q95N04; PRELIMINARY;
 AC Q95N04; PRELIMINARY;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DR Dihydrorollipamide acetyltransferase precursor (EC 2.3.1.12).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9833;
 RN [1]
 DR SEQUENCE FROM N.A.
 Schaffer R., Ramsey N., Samach A., Corden S., Putterill J., Carre I.A., Coupland G.; "The late elongated hypocotyl mutation of *Arabidopsis* disrupts circadian rhythms and the photoperiodic control of flowering." Cell 93:1129-1129 (1998).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
 DR EMBL; AA006404; CHA07004.1; -
 DR TRANSFAC; T02870; -
 DR GO; GO:0006334; C:nucleus; IEA.
 DR InterPro; IPR01005; Myb_DNA_binding.
 DR InterPro; IPR06447; Myb_SHQKYF.
 DR Pfam; PF00249; myb_DNA_binding; 1.
 DR SMART; SMC01717; SANT; 1.
 DR TIGRFAMs; TIGR01557; myb_SHQKYF; 1.

RESULT 29	[3]	RN	SEQUENCE FROM N.A.
Q9MAM8 PRELIMINARY; PRT; 656 AA.		RP	STRAIN=cv. B73;
ID Q9MAM8		RC	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
AC Q9MAM8		RA	Lilaca V., Linton E.W., Young S., Kovchoh S., Messing J.;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)		RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)		DR	EMBL; AF466646; AAL76206; 1.
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		DR	InterPro; IPR007321; Transposase; 28.
DB T25K16_6.		DR	PF04195; PF04195; Transpose; 28; 1.
OS Arabidopsis thaliana (Mouse-ear cress); Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		SQ	SEQUENCE 918 AA; 103639 MW; 111F4E95C34039495 CRC64;
RN [1]			
RP SEQUENCE FROM N.A.			Query Match 51.2%; Score 42; DB 10; Length 918;
RA Dunn P., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altaf H., Bei Q., Chin C., Chiu J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federer Spiel N.A., Theologis A., Ecker J.R.; RT "Genomic sequence for Arabidopsis thaliana BAC T25K16 from chromosome 1." Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		Best Local Similarity 87.5%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;	
RA [1]		RESULT 31	Matches 7; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
RA Q7UBG7 PRELIMINARY; PRT; 1120 AA.		Q7UBG7	SEQUENCE FROM N.A.
RA ID Q7UBG7; 25, Created)		AC	01-OCT-2003 (TREMBLrel. 25, Last sequence update)
RA DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.		DE	Hypothetical protein.
DR EMBL; AC007323; AAF26474.1; -		GN	RB6551.
DR GO; GO:0005634; C:nucleus; IEA.		OS	Rhodopirellula baltica.
DR GO; GO:0005677; F:DNA binding; IEA.		OC	Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planktomycteae; Pirellulidae.
DR InterPro; IPR001005; Myb DNA binding.		NCBI_TaxID=117;	OC
DR InterPro; IPR005447; Myb DNA binding.		[1]	Planktomycteae; Pirellulidae; Pirellulidae; Pirellulidae.
DR InterPro; IPR001005; Myb DNA binding; IEA.		RN	SEQUENCE FROM N.A.
DR InterPro; IPR001005; Myb DNA binding; IEA.		RC	STRAIN=1;
DR InterPro; IPR001005; Myb DNA binding; IEA.		RC	MEDLINE=22735913; PubMed=12835416;
DR InterPro; IPR001005; Myb DNA binding; IEA.		RX	Glockner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhard R.;
DR InterPro; IPR001005; Myb DNA binding; IEA.		RT	"Complete genome sequence of the marine planctomycete Pirellula sp. strain 1."
DR InterPro; IPR001005; Myb DNA binding; IEA.		RL	Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR InterPro; IPR001005; Myb DNA binding; IEA.		RC	STRAIN=1;
DR InterPro; IPR001005; Myb DNA binding; IEA.		RC	EMBL; BX94115; CAD7505; 1.
DR InterPro; IPR001005; Myb DNA binding; IEA.		DR	Hypothetical protein; Complete proteome.
DR InterPro; IPR001005; Myb DNA binding; IEA.		KW	Complete proteome.
DR InterPro; IPR001005; Myb DNA binding; IEA.		SEQUENCE	1120 AA; 123221 MW; 67C757B73421BP9B CRC64;
DR InterPro; IPR001005; Myb DNA binding; IEA.		Qy	Query Match 51.2%; Score 42; DB 16; Length 1120;
DR InterPro; IPR001005; Myb DNA binding; IEA.		Db	Best Local Similarity 70.0%; Pred. No. 1.8e+02; Mismatches 1; Indels 2; Gaps 0;
DR InterPro; IPR001005; Myb DNA binding; IEA.		Qy	2 AWYASRGIRP 11
DR InterPro; IPR001005; Myb DNA binding; IEA.		Db	206 AWWAAGIRP 215
RESULT 30			Query Match 51.2%; Score 42; DB 16; Length 1120;
Q8SA86 PRELIMINARY; PRT; 918 AA.		Best Local Similarity 70.0%; Pred. No. 1.8e+02; Mismatches 1; Indels 2; Gaps 0;	
ID Q8SA86		Q85712	SEQUENCE FROM N.A.
AC Q8SA86		AC	SEQUENCE FROM N.A.
DT 01-JUN-2002 (TREMBLrel. 21, Created)		DT	01-JUN-2003 (TREMBLrel. 24, Created)
DE Putative retrotransposon protein.		DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
OS Zea mays (Maize)		DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Pannicoideae; Andropogoneae; Zea.		DB	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
OX NCBI_TaxID=4577;		OS	Gp30.
RN SEQUENCE FROM N.A.		OS	Mycobacteriophage Bx22.
RC SPEAIN=cv. B73;		OC	Viruses; dsDNA viruses; no RNA stage; Caudovirales; Siphoviridae.
RA Ranakrishna W., Emberton J., SanMiguel P., Bennetzen J.; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		RN	SEQUENCE FROM N.A.
RN [12]		RP	SEQUENCE FROM N.A.
RA SEQUENCE FROM N.A.		RX	MEDLINE=22592610; PubMed=12705866;
RC STRAIN=cv. B73;		RA	Pedulla M.L., Ford M.E., Hourt J.M., Karthikayan T., Wadsworth C., Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Kumar V., Kandasamy J., Keenan L., Bardarov S., Brucker W., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W., Krikarov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Dooley J.; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		RA	

RN [1] SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Thymus;
 RC MEDLINE=23354683; PubMed=12466851;
 RX RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 67,770 full-length cDNAs.;"
 RT Nature 420:563-573 (2002).;
 RL DR AK083325; BAC36865.1; -;
 DR MGD; MGI:2443609; C920005C14Rik.
 DR InterPro; IPR001849; PH.
 DR PF00169; PH; 1.
 SMART: SM00233; PH; 1.
 PROSITE; PS5003; PH_DOMAIN; 1.
 RW PROTEIN; Hypothetical Protein.
 SQ SEQUENCE 259 AA; 28734 MW; 2B27DD35DFA0906 CRC64;
 Query Match 50.0%; Score 41; DB 11; Length 259;
 Best Local Similarity 87.5%; Pred. No. 56;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 RGIRPVGR 14
 Db 188 RGIRPVGR 195

RESULT 37
 Q8NSZ0 PRELIMINARY; PRT; 269 AA.
 AC Q8NSZ0;
 DT 01-OCT-2002 (TREMBLrel. 22; Created)
 DT 01-JUN-2003 (TREMBLrel. 22; Last sequence update)
 DE Aldo/keto reductases, related to diketogulonate reductase (EC 1.1.1.1-).
 DE C6H525.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.;"
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AP005215; BAA72198.1.
 DR GO:0016431; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001305; Aldo/ket red.
 DR PR00069; ALDKETREDTASB.
 DR PRODOM; PD000288; Aldo/ket red; 1.
 DR PF00248; Aldo/ket red; 1.
 DR PROSITE; PS00798; ALDKETOREDUCTASE_1.
 DR PROSITE; PS0062; ALDKETOREDUCTASE_2; 1.
 DR PROSITE; PS00063; ALDKETOREDUCTASE_3; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 269 AA; 30046 MW; F858A0130AB2891A CRC64;

Query Match 50.0%; Score 41; DB 16; Length 269;
 Best Local Similarity 53.8%; Pred. No. 58;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 210 AWYASRGIRPVGR 222

RESULT 38
 Q53929 PRELIMINARY; PRT; 276 AA.
 ID O53929;
 AC 053929;
 DT 01-OCT-2003 (TREMBLrel. 25; Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
 DE Conserved hypothetical protein.
 GN MB1744.
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinomycetales; Mycobacterium.
 OC Corynebacterineae; Corynebacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=AF2122; 97;
 RC MEDLINE=22709107; PubMed=12788972;
 RX Garnier T., Eigemeier K., Camus J. C., Medina N., Mansoor H.,

PRYOR M., Dutfoy S., Grondin S., Lacroix C., Monsempé C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Gordon R.G.,
 RT "The complete genome sequence of *Mycobacterium bovis*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8777-8782 (2003).
 DR EMBL; BX218340; CAD4447.1; -.
 KW Complete Proteome;
 SQ SEQUENCE 276 AA; 30015 MW; 9107C098AEB5C904 CRC64;
 Query Match 50.0%; Score 41; DB 16; Length 276;
 Best Local Similarity 45.5%; Pred. No. 60;
 Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 WYASRGIRPGV 13
 Db 150 WFAAKGVKAVG 160

RESULT 40

Q8YNR3 PRELIMINARY; PRT; 546 AA.
 ID Q8YNR3
 AC Q8YNR3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein Ali4499.
 GN Ali4499.
 OS *Anabaena* sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriuchi M., Itoh K., Kimura T.,
 RA Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpoo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete Genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium *Anabaena* sp. strain PCC 7120.";
 RL DNA Res. 8:205-213 (2001).
 DR EMBL; AP003596; BAB16198.1; -.
 DR PIR; AC2268; AC2368.
 DR InterPro; IPR001119; SLH.
 DR Pfam; PF00395; SLH; 1.
 DR PROSITE; PS01072; SLH; 1.
 DR HYPOTHETICAL PROTEIN; DOMAIN; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 546 AA; 58553 MW; 7A6A8E1961F72316 CRC64;
 Query Match 50.0%; Score 41; DB 16; Length 546;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
 Qy 2 AWY-ASRGIRPGV 14
 Db 457 AWYWAASIGRDFGR 477.

Search completed: February 25, 2004, 06:43:51
 Job time : 40 secs